



SEQUENCE LISTING

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<110> Huska Corporation
McCauley, Catherine A.
Tang, Liang A.

<120> COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE IL-13 RECEPTORS

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<140> 09/828,995

<141> 2001-04-09

<150> 60/195,874

<151> 2000-04-07

<150> 60/195,659

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<160> 104

<170> PatentIn version 3.1

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Pro

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Pro

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gacaccacc atg gag tct gtg ttc tgc tgg gtt ttc ctt gtc gtt att tta 111
 Met Glu Ser Val Phe Cys Trp Val Phe Leu Val Val Ile Leu
 1 5 10

aaa ggt gtc cag ggt gag gtg cag ttg gtg gag tct ggg gga gac ctg 159
 Lys Gly Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu
 15 20 25 30

gtg aag cct ggg ggg tcc ctg aga ctc tcc tgt gtg gcc tct gga ttc 207
 Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe
 35 40 45

acc ttc agt tcg tac tac atg cat tgg atc cgc cag gct cca ggg aag 255
 Thr Phe Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys
 50 55 60

ggg ctt cag cgg gtc gca cat att aga ggt gat gga agg act aca cac 303
 Gly Leu Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His
 65 70 75

tac gca gac gct atg aag ggc cga ttc acc atc tcc aga gac aac gcc 351
 Tyr Ala Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
 80 85 90

aag aac acg ctg tat ctg cag atg aat agc ctg aca gtc gaa gac acg 399
 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr
 95 100 105 110

gct att tat tac tgt gta aag gac ata tac tat ggg gtc ggg gac tat 447
 Ala Ile Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr
 115 120 125

tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc	495
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala	
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ccc tcg gtt ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc	543
Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser	
145 150 155	
acg gtg gcc ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta	591
Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val	
160 165 170	
act gtg tcc tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc	639
Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe	
175 180 185 190	
ccg tcc gtc ctg cag tcc tca ggg ctt cac tcc ctc agc agc atg gtg	687
Pro Ser Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val	
195 200 205	
aca gtg ccc tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg	735
Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val	
210 215 220	
gtc cac cca gcc agc aac act aaa gta gac aag cca gtg ttc aat gaa	783
Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu	
225 230 235	
tgc aga tgc act gat aca ccc cca tgc cca gtc cct gaa cct ctg gga	831
Cys Arg Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly	
240 245 250	
ggg cct tcg gtc ctc atc ttt ccc ccg aaa ccc aag gac atc ctc agg	879
Gly Pro Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg	
255 260 265 270	
att acc cga aca ccc gag gtc acc tgt gtg gtg tta gat ctg ggc cgt	927
Ile Thr Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg	
275 280 285	
gag gac cct gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg	975
Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val	
290 295 300	
cac aca gcc aag acc cag tct cgt gag cag cag ttc aac ggc acc tac	1023
His Thr Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr	
305 310 315	
cgt gtg gtc agc gtc ctc ccc att gag cac cag gac tgg ctc aca ggg	1071
Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly	
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Lys Glu Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile	
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gag agg acc atc tct aag gcc aga ggg agg gcc cat aag ccc agt gtg 1167
 Glu Arg Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val
 355 360 365

tat gtc ctg ccg cca tcc cca aag gag ttg tca tcc agt gac aca gtc 1215
 Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val
 370 375 380

agc atc acc tgc ctg ata aaa gac ttc tac cca cct gac att gat gtg 1263
 Ser Ile Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val
 385 390 395

gag tgg cag agc aat gga cag cag gag ccc gag agg aag cac cgc atg 1311
 Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met
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acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag 1359
 Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
 415 420 425 430

ctc tct gtg gac aag agc cgc tgg cag cag gga gac ccc ttc aca tgt 1407
 Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys
 435 440 445

gcg gtg atg cat gaa act cta cag aac cac tac aca gat cta tcc ctc 1455
 Ala Val Met His Glu Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu
 450 455 460

tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc 1503
 Ser His Ser Pro Gly Lys
 465

cccacccttg gctctcagga tcccctgagg acacctgagc ccctgtccct gtgtacataa 1563

ccctgggtag gcacccatca tgaaataaag caccagcac tgccctgggc cctgcaaaaa 1623

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1654

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 <213> Canis familiaris

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Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Ser Tyr Tyr Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Gln Arg Val Ala His Ile Arg Gly Asp Gly Arg Thr Thr His Tyr Ala
65 70 75 80

Asp Ala Met Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Thr Val Glu Asp Thr Ala Ile
100 105 110

Tyr Tyr Cys Val Lys Asp Ile Tyr Tyr Gly Val Gly Asp Tyr Trp Gly
115 120 125

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser
130 135 140

Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val
145 150 155 160

Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val
165 170 175

Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser
180 185 190

Val Leu Gln Ser Ser Gly Leu His Ser Leu Ser Ser Met Val Thr Val
195 200 205

Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His
210 215 220

Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg
225 230 235 240

Cys Thr Asp Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro
245 250 255

Ser Val Leu Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr
260 265 270

Arg Thr Pro Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp
275 280 285

Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr
290 295 300

Ala Lys Thr Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val
305 310 315 320

Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu
325 330 335

Phe Lys Cys Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg
340 345 350

Thr Ile Ser Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val
355 360 365

Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile
370 375 380

Thr Cys Leu Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp
385 390 395 400

Gln Ser Asn Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro
405 410 415

Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser
420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val
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Met His Glu Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His
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Ser Pro Gly Lys
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 tgttgctggc tgggtggacc acgttgacgg tgaaggtctc gctggggccac ctgctggagg 960
 gcactgtcac catgctgctg agggagtga gacctgagga ctgcaggacg gacgggaagg 1020
 tgtgcacacc gctgggtcaag gagccggaat tccaggacac agttacaggc tcggggaagt 1080
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 tgggtgaatcg gcccttcata gcgtctgcgt agtgtgtagt ccttccatca cctctaatat 1380
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 Ser

<210> 8
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 Pro Lys Glu Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu
 1 5 10 15
 Ser

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Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly		
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gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg		152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly		
20 25 30 35		
tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat		200
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr		
40 45 50		
ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc		248
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val		
55 60 65		
gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag		296
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys		
70 75 80		
ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc		344
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu		
85 90 95		
cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg		392
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val		
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Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn		
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Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val		
135 140 145		
ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc		536
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala		
150 155 160		
ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc		584
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser		
165 170 175		
tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc		632
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val		
180 185 190 195		
ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc		680
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro		
200 205 210		

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Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro	
215 220 225	
gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc	776
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys	
230 235 240	
aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg	824
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser	
245 250 255	
gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga	872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg	
260 265 270 275	
aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct	920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro	
280 285 290	
gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc	968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala	
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Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val	
310 315 320	
agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc	1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe	
325 330 335	
aag tgc aga gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act	1112
Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr	
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Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu	
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Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr	
375 380 385	
tgc ctg atc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag	1256
Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln	
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Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro	
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cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg	1352
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val	
420 425 430 435	
gac aag agc cgc tgg cag cag gga gac acc ttc aca tgt gcg gtg atg	1400

Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met
 440 445 450

cat gaa gct cta cag aac cac tac aca gat cta tcc ctc tcc cat tct 1448
 His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser
 455 460 465

ccg ggt aaa tga 1460
 Pro Gly Lys
 470

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 <213> Canis familiaris

<400> 11

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 20 25 30

Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
 35 40 45

Ser Asp Tyr Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
 50 55 60

Gln Trp Val Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp
 65 70 75 80

Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
 85 90 95

Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr
 100 105 110

His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His
 115 120 125

Trp Gly Asn Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala
 130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
 145 150 155 160

Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val
195 200 205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
210 215 220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu
225 230 235 240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly
245 250 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
260 265 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg
275 280 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val
290 295 300

His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr
305 310 315 320

Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly
325 330 335

Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile
340 345 350

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
355 360 365

Tyr Val Leu Pro Pro Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val
370 375 380

Thr Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val
385 390 395 400

Glu Trp Gln Ser Asn Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr
405 410 415

Thr Ala Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys
420 425 430

Leu Ser Val Asp Lys Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys
435 440 445

Ala Val Met His Glu Ala Leu Gln Asn His Tyr Thr Asp Leu Ser Leu
450 455 460

Ser His Ser Pro Gly Lys
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gctaacagct gcgaccact gcagcccctt ccctggagac tgacggaccc aactcatgcc      1260
atagtcaact aaggtgaatc cagaggccac acaggacagt ctcaaggacc cccaggtt      1320
caccaggtct ccccgagact ccaccagttg cacctaccc tggacacctt ttaaaataga      1380
gacaaggaaa acccagcaga gcacagactc catggtggtt tgtctgtgtt gtgtcctgag      1440
cactgaatgg ggtcacctgg                                         1460

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<210> 13
<211> 60
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(60)
<223>

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<400> 13
gcc aaa gaa tgc gag tgc aag tgt aac tgt aac aac tgc cca tgc cca      48
Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
1          5          10          15

ggt tgt ggc ctg                                         60
Gly Cys Gly Leu
20

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<210> 14
<211> 20
<212> PRT
<213> Canis familiaris

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<400> 14
Ala Lys Glu Cys Glu Cys Lys Cys Asn Cys Asn Asn Cys Pro Cys Pro
1          5          10          15

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Gly Cys Gly Leu
20

<210> 15
<211> 60
<212> DNA
<213> Canis familiaris

<400> 15
caggccacaa cctgggcatg ggcagttggt acagttacac ttgcactcgc attctttggc 60

<210> 16
<211> 1456
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (32)..(1453)
<223>

<220>
<221> misc_feature
<222> (27)..(27)
<223> At nucleotide 27, n = unknown

<400> 16
aagtgtcag gcacaacaca gacaaancac c atg gag tct gtg ctc tac tgg 52
Met Glu Ser Val Leu Tyr Trp
1 5

gtt ttc ctt gtc gct att tta aag ggt gtc cag ggt gac gtg cag ctg 100
Val Phe Leu Val Ala Ile Leu Lys Gly Val Gln Gly Asp Val Gln Leu
10 15 20

gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg tcc ttg aga ctg 148
Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly Ser Leu Arg Leu
25 30 35

tcc tgt gtg gcc tct gga ttc acc ttt agt agc tgt gcc atg agc tgg 196
Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Ser Cys Ala Met Ser Trp
40 45 50 55

gtc cgt cag tct cca ggg aag ggg cct cag tgg gtc gca act att cgg 244
Val Arg Gln Ser Pro Gly Lys Gly Pro Gln Trp Val Ala Thr Ile Arg
60 65 70

tat gat gga agt gat ata tac tac gca gac gct gtg aag ggc cga ttc 292
Tyr Asp Gly Ser Asp Ile Tyr Tyr Ala Asp Ala Val Lys Gly Arg Phe
75 80 85

agc atc tcc aga gac aac gcc aag aac acg gtg tat ctg cag atg aac 340
Ser Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln Met Asn

90	95	100	
agc ctg aga gcc gag gac acg gcc gtg tat tat tgt gcg aag gcc ccc Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ala Pro 105 110 115			388
ccc tac gat agt tac cac tat ggt atg gac tat tgg ggt cct ggc act Pro Tyr Asp Ser Tyr His Tyr Gly Met Asp Tyr Trp Gly Pro Gly Thr 120 125 130 135			436
tcc ctc ttc gtg tcg tca gcc tcc acc acg gcc ccc tcg gtt ttc cca Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro 140 145 150			484
ctg gcc ccc agc tgt ggg tcc caa tcc ggc tcc acg gtg gcc ctg gcc Leu Ala Pro Ser Cys Gly Ser Gln Ser Gly Ser Thr Val Ala Leu Ala 155 160 165			532
tgc ctg gtg tca ggc tac atc ccc gag cct gta act gtg tcc tgg aat Cys Leu Val Ser Gly Tyr Ile Pro Glu Pro Val Thr Val Ser Trp Asn 170 175 180			580
tcc gtc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag Ser Val Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln 185 190 195			628
tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc tcc agc Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro Ser Ser 200 205 210 215			676
agg tgg ccc agc gag acc ttc acc tgc aat gtg gcc cac ccg gcc acc Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro Ala Thr 220 225 230			724
aac act aaa gta gac aag cca gtg gcc aaa gaa tgc gag tgc aag tgt Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys 235 240 245			772
aac tgt aac aac tgc cca tgc cca ggt tgt ggc ctg ctg gga ggg cct Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro 250 255 260			820
tcg gtc ttc atc ttt ccc cca aaa ccc aag gac atc ctc gtg act gcc Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala 265 270 275			868
cgg aca ccc aca gtc act tgt gtg gtg gtg gat ctg gac cca gaa aac Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn 280 285 290 295			916
cct gag gtg cag atc agc tgg ttc gtg gat agt aag cag gtg caa aca Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr 300 305 310			964
gcc aac acg cag cct cgt gag gag cag tcc aat ggc acc tac cgt gtg Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val 315 320 325			1012

gtc agt gtc ctc ccc att ggg cac cag gac tgg ctt tca ggg aag cag	1060
Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln	
330 335 340	
ttc aag tgc aaa gtc aac aac aaa gcc ctc cca tcc ccc att gag gag	1108
Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu	
345 350 355	
atc atc tcc aag acc cca ggg cag gcc cat cag cct aat gtg tat gtc	1156
Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val	
360 365 370 375	
ctg ccg cca tgc cgg gat gag atg agc aag aat acg gtc acc ctg acc	1204
Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr	
380 385 390	
tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag	1252
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln	
395 400 405	
agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc	1300
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro	
410 415 420	
cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg	1348
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val	
425 430 435	
gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg	1396
Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met	
440 445 450 455	
cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct	1444
His Glu Ala Leu His Asn His Tyr Thr Gln Ile Ser Leu Ser His Ser	
460 465 470	
ccg ggt aaa tga	1456
Pro Gly Lys	

<210> 17
 <211> 474
 <212> PRT
 <213> Canis familiaris

<400> 17

Met Glu Ser Val Leu Tyr Trp Val Phe Leu Val Ala Ile Leu Lys Gly
1 5 10 15

Val Gln Gly Asp Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30

Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Thr	Phe	
		35					40					45				
Ser	Ser	Cys	Ala	Met	Ser	Trp	Val	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Pro	
	50					55					60					
Gln	Trp	Val	Ala	Thr	Ile	Arg	Tyr	Asp	Gly	Ser	Asp	Ile	Tyr	Tyr	Ala	
65					70					75					80	
Asp	Ala	Val	Lys	Gly	Arg	Phe	Ser	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
				85					90					95		
Thr	Val	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	
			100					105					110			
Tyr	Tyr	Cys	Ala	Lys	Ala	Pro	Pro	Tyr	Asp	Ser	Tyr	His	Tyr	Gly	Met	
		115					120					125				
Asp	Tyr	Trp	Gly	Pro	Gly	Thr	Ser	Leu	Phe	Val	Ser	Ser	Ala	Ser	Thr	
	130					135					140					
Thr	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Cys	Gly	Ser	Gln	Ser	
145					150					155					160	
Gly	Ser	Thr	Val	Ala	Leu	Ala	Cys	Leu	Val	Ser	Gly	Tyr	Ile	Pro	Glu	
				165				170						175		
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Val	Ser	Leu	Thr	Ser	Gly	Val	His	
			180					185					190			
Thr	Phe	Pro	Ser	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	
		195					200					205				
Met	Val	Thr	Val	Pro	Ser	Ser	Arg	Trp	Pro	Ser	Glu	Thr	Phe	Thr	Cys	
	210					215					220					
Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Ala	
225					230					235					240	
Lys	Glu	Cys	Glu	Cys	Lys	Cys	Asn	Cys	Asn	Asn	Cys	Pro	Cys	Pro	Gly	
				245					250					255		
Cys	Gly	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	

260	265	270
Lys Asp Ile Leu Val Thr Ala Arg Thr Pro Thr Val Thr Cys Val Val		
275	280	285
Val Asp Leu Asp Pro Glu Asn Pro Glu Val Gln Ile Ser Trp Phe Val		
290	295	300
Asp Ser Lys Gln Val Gln Thr Ala Asn Thr Gln Pro Arg Glu Glu Gln		
305	310	315 320
Ser Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln		
	325	330 335
Asp Trp Leu Ser Gly Lys Gln Phe Lys Cys Lys Val Asn Asn Lys Ala		
	340	345 350
Leu Pro Ser Pro Ile Glu Glu Ile Ile Ser Lys Thr Pro Gly Gln Ala		
	355	360 365
His Gln Pro Asn Val Tyr Val Leu Pro Pro Ser Arg Asp Glu Met Ser		
	370	375 380
Lys Asn Thr Val Thr Leu Thr Cys Leu Val Lys Asp Phe Phe Pro Pro		
385	390	395 400
Glu Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser		
	405	410 415
Lys Tyr Arg Met Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe		
	420	425 430
Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp		
	435	440 445
Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr		
	450	455 460
Gln Ile Ser Leu Ser His Ser Pro Gly Lys		
465	470	

<210> 18
 <211> 1456

<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (1430)..(1430)
<223> At nucleotide 1430, n = unknown

<400> 18
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gctgtatagg aagtaggacc catcttcate cagctggggc ggggtcatgc ggtacttgct 180
ctcaggctcc tgctgtccat tgctctgcca ctccacatca atctcagggtg ggaagaagtc 240
tttgaccaga caggtcaggg tgaccgtatt cttgctcate tcatcccgcg atggcggcag 300
gacatacaca ttaggctgat gggcctgccc tggggctctt gagatgatct cctcaatggg 360
ggatgggagg gctttgttgt tgactttgca cttgaactgc ttccctgaaa gccagtcctg 420
gtgccaatg gggaggacac tgaccacacg gtaggtgcca ttggactgct cctcacgagg 480
ctgcgtgttg gctgtttgca cctgcttact atccacgaac cagctgatct gcacctcagg 540
gttttctggg tccagatcca ccaccacaca agtgactgtg ggtgtccggg cagtcacgag 600
gatgtccttg ggttttgggg gaaagatgaa gaccgaaggc cctcccagca ggccacaacc 660
tgggcatggg cagttgttac agttacactt gcaactcgcat tctttggcca ctggcttgtc 720
tacttttagtg ttggtggccg ggtgggccac attgcagggtg aaggtctcgc tggggcacct 780
gctggagggc actgtcacca tgctgctgag ggagtagagc cctgaggact gcaggacgga 840
cgggaagggtg tgcacaccgc tggtaagga gacggaattc caggacacag ttacaggctc 900
ggggatgtag cctgacacca ggcaggccag ggccaccgtg gagccggatt gggaccaca 960
gctggggggc agtgggaaaa ccgagggggc cgtggtggag gctgacgaca cgaagaggga 1020
agtgccagga cccaatagt ccataccata gtggtaacta tcgtaggggg gggccttcgc 1080
acaataatac acggcctgtt cctcggtctt caggctgttc atctgcagat acaccgtgtt 1140
cttggcgttg tctctggaga tgctgaatcg gcccttcaca gcgtctgcgt agtatatata 1200
acttccatca taccgaatag ttgcgaccca ctgaggcccc ttccctggag actgacggac 1260
ccagctcatg gcacagctac taaagggtgaa tccagaggcc acacaggaca gtctcaagga 1320
ccccccaggc ttcaccaggt ctccccaga ctccaccagc tgcacgtcac cctggacacc 1380
ctttaaaata gcgacaagga aaaccagta gagcacagac tccatggtgn tttgtctgtg 1440

ttgtgcctga gcactt

1456

<210> 19
<211> 1453
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (32)..(1450)
<223>

<400> 19

agtgtcagg acaccacaca gacaaatcac c atg gag tct gtg ctc ttc tgg 52
Met Glu Ser Val Leu Phe Trp
1 5

gtt ttc ctt gtc act att tta aaa ggt gtc cag ggt gag gta cgt ttg 100
Val Phe Leu Val Thr Ile Leu Lys Gly Val Gln Gly Glu Val Arg Leu
10 15 20

gtg gag tct gga gga acc ctg gtg aag cct ggg ggg tcc ctg aaa ctc 148
Val Glu Ser Gly Gly Thr Leu Val Lys Pro Gly Gly Ser Leu Lys Leu
25 30 35

tct tgt gtg gcc tct gga ttc acc ttc aga aga tac tcc atg gac tgg 196
Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Arg Tyr Ser Met Asp Trp
40 45 50 55

gtc cgc cag gct cca ggc aag agc ctg cag tgg gtc gcc ggg att aac 244
Val Arg Gln Ala Pro Gly Lys Ser Leu Gln Trp Val Ala Gly Ile Asn
60 65 70

ggt gat ggc aca gga aca tcc tat tca cag act gtg aag ggc cga ttc 292
Gly Asp Gly Thr Gly Thr Ser Tyr Ser Gln Thr Val Lys Gly Arg Phe
75 80 85

acc atc tcc aga gac aac gcc aag aac acc ctc tat ctg cag ata aac 340
Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Ile Asn
90 95 100

agc ctg aga gcc gaa gac tct gct gtg tat tat tgt gcc aag agc tgg 388
Ser Leu Arg Ala Glu Asp Ser Ala Val Tyr Tyr Cys Ala Lys Ser Trp
105 110 115

tct cgt aat ggg gat ctt gac tac tgg ggc cag gga acc ctg gtc acc 436
Ser Arg Asn Gly Asp Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
120 125 130 135

gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg gcc ccc 484
Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu Ala Pro
140 145 150

agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc ctg gtg 532

Ser	Cys	Gly	Ser	Thr	Ser	Gly	Ser	Thr	Val	Ala	Leu	Ala	Cys	Leu	Val	
			155					160					165			
tca	ggc	tac	ttc	ccc	gag	cct	gta	act	gtg	tcc	tgg	aat	tcc	ggc	tcc	580
Ser	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ser	
		170					175					180				
ttg	acc	agc	ggt	gtg	cac	acc	ttc	ccg	tcc	gtc	ctg	cag	tcc	tca	ggg	628
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ser	Val	Leu	Gln	Ser	Ser	Gly	
	185					190					195					
ctc	tac	tcc	ctc	agc	agc	atg	gtg	aca	gtg	ccc	tcc	agc	agg	tgg	ccc	676
Leu	Tyr	Ser	Leu	Ser	Ser	Met	Val	Thr	Val	Pro	Ser	Ser	Arg	Trp	Pro	
200					205					210					215	
agc	gag	acc	ttc	acc	tgc	aac	gtg	gcc	cac	ccg	gcc	agc	aaa	act	aaa	724
Ser	Glu	Thr	Phe	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser	Lys	Thr	Lys	
				220					225					230		
gta	gac	aag	cca	gtg	ccc	aaa	aga	gaa	aat	gga	aga	gtt	cct	cgc	cca	772
Val	Asp	Lys	Pro	Val	Pro	Lys	Arg	Glu	Asn	Gly	Arg	Val	Pro	Arg	Pro	
			235					240					245			
cct	gat	tgt	ccc	aaa	tgc	cca	gcc	cct	gaa	atg	ctg	gga	ggg	cct	tcg	820
Pro	Asp	Cys	Pro	Lys	Cys	Pro	Ala	Pro	Glu	Met	Leu	Gly	Gly	Pro	Ser	
		250					255					260				
gtc	ttc	atc	ttt	ccc	ccg	aaa	ccc	aag	gac	acc	ctc	ttg	att	gcc	cga	868
Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Leu	Ile	Ala	Arg	
	265					270					275					
aca	cct	gag	gtc	aca	tgt	gtg	gtg	gtg	gat	ctg	gac	cca	gaa	gac	cct	916
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Leu	Asp	Pro	Glu	Asp	Pro	
280					285					290					295	
gag	gtg	cag	atc	agc	tgg	ttc	gtg	gac	ggg	aag	cag	atg	caa	aca	gcc	964
Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	Gln	Met	Gln	Thr	Ala	
				300					305					310		
aag	act	cag	cct	cgt	gag	gag	cag	ttc	aat	ggc	acc	tac	cgt	gtg	gtc	1012
Lys	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Gly	Thr	Tyr	Arg	Val	Val	
			315					320					325			
agt	gtc	ctc	ccc	att	ggg	cac	cag	gac	tgg	ctc	aag	ggg	aag	cag	ttc	1060
Ser	Val	Leu	Pro	Ile	Gly	His	Gln	Asp	Trp	Leu	Lys	Gly	Lys	Gln	Phe	
		330					335					340				
acg	tgc	aaa	gtc	aac	aac	aaa	gcc	ctc	cca	tcc	ccg	atc	gag	agg	acc	1108
Thr	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ser	Pro	Ile	Glu	Arg	Thr	
	345					350					355					
atc	tcc	aag	gcc	aga	ggg	caa	gcc	cat	cag	ccc	agt	gtg	tat	gtc	ctg	1156
Ile	Ser	Lys	Ala	Arg	Gly	Gln	Ala	His	Gln	Pro	Ser	Val	Tyr	Val	Leu	
360					365					370					375	
ccg	cca	tcc	cgg	gag	gag	ttg	agc	aag	aac	aca	gtc	agc	ttg	aca	tgc	1204
Pro	Pro	Ser	Arg	Glu	Glu	Leu	Ser	Lys	Asn	Thr	Val	Ser	Leu	Thr	Cys	

	380	385	390	
ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag tgg cag agc				1252
Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu Trp Gln Ser				
	395	400	405	
aat gga cag cag gag cct gag agc aag tac cgc acg acc ccg ccc cag				1300
Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln				
	410	415	420	
ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac				1348
Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp				
	425	430	435	
aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg cat				1396
Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met His				
	440	445	450	455
gaa gct cta cac aac cac tac aca cag gaa tcc ctc tcc cat tct ccg				1444
Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser His Ser Pro				
	460	465	470	
ggt aaa tga				1453
Gly Lys				

<210> 20
 <211> 473
 <212> PRT
 <213> Canis familiaris
 <400> 20

Met Glu Ser Val Leu Phe Trp Val Phe Leu Val Thr Ile Leu Lys Gly			
1	5	10	15
Val Gln Gly Glu Val Arg Leu Val Glu Ser Gly Gly Thr Leu Val Lys			
	20	25	30
Pro Gly Gly Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe			
	35	40	45
Arg Arg Tyr Ser Met Asp Trp Val Arg Gln Ala Pro Gly Lys Ser Leu			
	50	55	60
Gln Trp Val Ala Gly Ile Asn Gly Asp Gly Thr Gly Thr Ser Tyr Ser			
65	70	75	80
Gln Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn			
	85	90	95

Thr Leu Tyr Leu Gln Ile Asn Ser Leu Arg Ala Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Ala Lys Ser Trp Ser Arg Asn Gly Asp Leu Asp Tyr Trp
 115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro
 130 135 140

Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr
 145 150 155 160

Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr
 165 170 175

Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190

Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr
 195 200 205

Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala
 210 215 220

His Pro Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu
 225 230 235 240

Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro
 245 250 255

Glu Met Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys
 260 265 270

Asp Thr Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val
 275 280 285

Asp Leu Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp
 290 295 300

Gly Lys Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe
 305 310 315 320

Asn Gly Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp
325 330 335

Trp Leu Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu
340 345 350

Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His
355 360 365

Gln Pro Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys
370 375 380

Asn Thr Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp
385 390 395 400

Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys
405 410 415

Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu
420 425 430

Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr
435 440 445

Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
450 455 460

Glu Ser Leu Ser His Ser Pro Gly Lys
465 470

<210> 21
<211> 1453
<212> DNA
<213> Canis familiaris

<400> 21
tcatttaccc ggagaatggg agagggattc ctgtgtgtag tggttgtgta gagcttcatg 60
catcaccgca catatgaagg tgtctccccg ctgccagcgg ctcttgtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180
ctcagggtcc tgctgtccat tgctctgcca ctccacatca atgtcagggtg ggaagaagtc 240
tttgatcagg catgtcaagc tgactgtgtt cttgctcaac tcctcccggg atggcggcag 300
gacatacaca ctgggctgat gggcttgccc tctggccttg gagatgggtc tctcgatcgg 360

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ggatgggagg gctttgttgt tgactttgca cgtgaactgc ttcccccttga gccagtctctg 420
gtgccaatg gggaggacac tgaccacacg gtaggtgcca ttgaactgct cctcacgagg 480
ctgagtcttg gctgtttgca tctgcttacc gtccacgaac cagctgatct gcacctcagg 540
gtcttctggg tccagatcca ccaccacaca tgtgacctca ggtgttcggg caatcaagag 600
ggtgtccttg ggtttcgggg gaaagatgaa gaccgaaggc cctcccagca tttcaggggc 660
tgggcatttg ggacaatcag gtgggcgagg aactcttcca ttttctcttt tgggcactgg 720
cttgtctact ttagttttgc tggccgggtg ggccacgttg caggtgaagg tctcgctggg 780
ccacctgctg gagggcactg tcaccatgct gctgaggag tagagccctg aggactgcag 840
gacggacggg aaggtgtgca caccgctggt caaggagccg gaattccagg acacagttac 900
aggctcgggg aagtagcctg acaccaggca ggccagggcc accgtggagc cggaagtgga 960
cccgcagctg ggggccagtg ggaaaaccga gggggccgtg gtggaggctg aggagacggt 1020
gaccaggggt ccttggtccc agtagtcaag atccccatta cgagaccagc tcttggcaca 1080
ataatacaca gcagagtctt cggctctcag gctgtttatc tgcagataga ggggtgttctt 1140
ggcgttgtct ctggagatgg tgaatcgcc cttcacagtc tgtgaatagg atgttctgt 1200
gccatcacg ttaatcccg cgacctactg caggctcttg cctggagcct ggcggaacca 1260
gtccatggag tatcttctga aggtgaatcc agaggccaca caagagagtt tcagggaccc 1320
cccaggcttc accagggttc ctccagactc caccaaactg acctcaccct ggacaccttt 1380
taaaatagtg acaaggaaaa ccagaagag cacagactcc atggtgattt gtctgtgtgg 1440
tgtctgagc act 1453

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<210> 22
<211> 66
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(66)
<223>

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<400> 22
ccc aaa aga gaa aat gga aga gtt cct cgc cca cct gat tgt ccc aaa 48
Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
1 5 10 15
tgc cca gcc cct gaa atg 66

```

Cys Pro Ala Pro Glu Met
20

<210> 23
<211> 22
<212> PRT
<213> Canis familiaris

<400> 23

Pro Lys Arg Glu Asn Gly Arg Val Pro Arg Pro Pro Asp Cys Pro Lys
1 5 10 15

Cys Pro Ala Pro Glu Met
20

<210> 24
<211> 66
<212> DNA
<213> Canis familiaris

<400> 24
catttcaggg gctgggcatt tgggacaatc aggtgggcga ggaactcttc cattttctct 60
tttggg 66

<210> 25
<211> 938
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (37)..(753)
<223>

<220>
<221> misc_feature
<222> (475)..(475)
<223> At nucleotide 475, n = unknown
At amino acid residue 147, Xaa = Pro, Ser, Ala or Thr

<220>
<221> misc_feature
<222> (479)..(479)
<223> At nucleotide 479, y = c or t;
At amino acid residue 148, Xaa = Ser or Phe

<220>
<221> misc_feature

<222> (482)..(482)
 <223> At nucleotide 482, y = c or t;
 At amino acid residue 149, Xaa = Ser or Phe

<220>
 <221> misc_feature
 <222> (542)..(542)
 <223> At nucleotide 542, r = a or g;
 At amino acid residue 169, Xaa = Asn or Ser

<400> 25
 ggcacgaggg tccccagaag gcaggatcaa tcagtg atg tcc tcc gac atg gcc 54
 Met Ser Ser Asp Met Ala
 1 5

tgg tcc cct ctc ctc ctc aca ctc ctc gct cac tgc aca ggg tcc tgg 102
 Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys Thr Gly Ser Trp
 10 15 20

gcc cag gct gtg ttg aat cag ccg gcc tca gta tct ggg gcc ctg ggc 150
 Ala Gln Ala Val Leu Asn Gln Pro Ala Ser Val Ser Gly Ala Leu Gly
 25 30 35

cag aag gtc acc atc tcc tgc tct gga gac acg aat gac att gat ata 198
 Gln Lys Val Thr Ile Ser Cys Ser Gly Asp Thr Asn Asp Ile Asp Ile
 40 45 50

ttc ggt gtg aac tgg tac caa caa ctc cca gga aag gcc cct aca gtc 246
 Phe Gly Val Asn Trp Tyr Gln Gln Leu Pro Gly Lys Ala Pro Thr Val
 55 60 65 70

ctc gtg gac agt gat ggg gat cga ccc tca ggg gtc cct gac aga ttt 294
 Leu Val Asp Ser Asp Gly Asp Arg Pro Ser Gly Val Pro Asp Arg Phe
 75 80 85

tct ggc tcc agt tct ggc aac tca ggc acc ctg acc atc act ggg ctc 342
 Ser Gly Ser Ser Ser Gly Asn Ser Gly Thr Leu Thr Ile Thr Gly Leu
 90 95 100

cag gct gag gac gag gct gat tat tac tgt cag tct gtt gat tcc acg 390
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Val Asp Ser Thr
 105 110 115

ctt ggt gtt tac gtg ttc ggc tca gga acc caa ctg act gtc ctt ggt 438
 Leu Gly Val Tyr Val Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Gly
 120 125 130

cag ccc aag gcc tcc ccc tcg gtc aca ctc ttc ccg ncc tyc tyt gag 486
 Gln Pro Lys Ala Ser Pro Ser Val Thr Leu Phe Pro Xaa Xaa Xaa Glu
 135 140 145 150

gag ctc ggc gcc aac aag gcc acc ctg gtg tgc ctc atc agc gac ttc 534
 Glu Leu Gly Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 155 160 165

tac ccc arc ggc gtg acg gtg gcc tgg aag gca gac ggc agc ccc gtc	582
Tyr Pro Xaa Gly Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val	
170 175 180	
acc cag ggc gtg gag acc acc aag ccc tcc aag cag agc aac aac aag	630
Thr Gln Gly Val Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys	
185 190 195	
tac gcg gcc agc agc tac ctg agc ctg acg cct gac aag tgg aaa tct	678
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Asp Lys Trp Lys Ser	
200 205 210	
cac agc agc ttc agc tgc ctg gtc acg cat gag ggg agc ccc gtg gaa	726
His Ser Ser Phe Ser Cys Leu Val Thr His Glu Gly Ser Pro Val Glu	
215 220 225 230	
aaa aag gtg gcc ccc gca aag tgc tct taggttcccg atgccccccg	773
Lys Lys Val Ala Pro Ala Lys Cys Ser	
235	
cccaccaaag ggggctcaaa gcctcaggac ctccaggagg atcttgccctc ccattctgggt	833
catcccagcc attcccctta aaccagcgca acattcaata aagtgttctt tcttcaatca	893
gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa	938

<210> 26
 <211> 239
 <212> PRT
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (147)..(147)
 <223> The 'Xaa' at location 147 stands for Thr, Ala, Pro, or Ser.

<220>
 <221> misc_feature
 <222> (148)..(148)
 <223> The 'Xaa' at location 148 stands for Ser, or Phe.

<220>
 <221> misc_feature
 <222> (149)..(149)
 <223> The 'Xaa' at location 149 stands for Ser, or Phe.

<220>
 <221> misc_feature
 <222> (169)..(169)
 <223> The 'Xaa' at location 169 stands for Ser, or Asn.

<400> 26

Met Ser Ser Asp Met Ala Trp Ser Pro Leu Leu Thr Leu Leu Ala
1 5 10 15

His	Cys	Thr	Gly	Ser	Trp	Ala	Gln	Ala	Val	Leu	Asn	Gln	Pro	Ala	Ser			
			20					25					30					
Val	Ser	Gly	Ala	Leu	Gly	Gln	Lys	Val	Thr	Ile	Ser	Cys	Ser	Gly	Asp			
		35					40					45						
Thr	Asn	Asp	Ile	Asp	Ile	Phe	Gly	Val	Asn	Trp	Tyr	Gln	Gln	Leu	Pro			
	50					55					60							
Gly	Lys	Ala	Pro	Thr	Val	Leu	Val	Asp	Ser	Asp	Gly	Asp	Arg	Pro	Ser			
65					70					75					80			
Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Asn	Ser	Gly	Thr			
				85					90					95				
Leu	Thr	Ile	Thr	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys			
			100					105					110					
Gln	Ser	Val	Asp	Ser	Thr	Leu	Gly	Val	Tyr	Val	Phe	Gly	Ser	Gly	Thr			
		115					120					125						
Gln	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ser	Pro	Ser	Val	Thr	Leu			
	130					135					140							
Phe	Pro	Xaa	Xaa	Xaa	Glu	Glu	Leu	Gly	Ala	Asn	Lys	Ala	Thr	Leu	Val			
145					150					155					160			
Cys	Leu	Ile	Ser	Asp	Phe	Tyr	Pro	Xaa	Gly	Val	Thr	Val	Ala	Trp	Lys			
				165					170					175				
Ala	Asp	Gly	Ser	Pro	Val	Thr	Gln	Gly	Val	Glu	Thr	Thr	Lys	Pro	Ser			
			180					185					190					
Lys	Gln	Ser	Asn	Asn	Lys	Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr			
	195						200					205						
Pro	Asp	Lys	Trp	Lys	Ser	His	Ser	Ser	Phe	Ser	Cys	Leu	Val	Thr	His			
	210					215					220							
Glu	Gly	Ser	Pro	Val	Glu	Lys	Lys	Val	Ala	Pro	Ala	Lys	Cys	Ser				
225					230					235								

<210> 27
 <211> 938
 <212> DNA
 <213> Canis familiaris

<220>
 <221> misc_feature
 <222> (464)..(464)
 <223> At nucleotide 464, n = unknown

<400> 27
 tttttttttt tttttttttt tttttttttt tttttttttt ttttctgatt gaagaaagaa 60
 cactttattg aatgttgcct gggtttaagg ggaatggctg ggatgacca gatgggaggc 120
 aagatcctcc tggaggtcct gaggctttga gccccctttg gtgggcgggg ggcacgcgga 180
 acctaagagc actttgcggg ggccaccttt ttttccacgg ggctcccctc atgcgtgacc 240
 aggcagctga agctgctgtg agatttccac ttgtcaggcg tcaggctcag gtagctgctg 300
 gccgcgtact tgttgttgct ctgcttgag ggcttggtgg tctccacgcc ctgggtgacg 360
 gggctgccgt ctgccttcca ggccaccgtc acgccgytgg ggtagaagtc gctgatgagg 420
 cacaccaggg tggccttggt ggccgccgagc tcctcaragr aggnccggaa gagtgtgacc 480
 gagggggagg ccttgggctg accaaggaca gtcagttggg ttcctgagcc gaacacgtaa 540
 acaccaagcg tggaatcaac agactgacag taataatcag cctcgtcctc agcctggagc 600
 ccagtgatgg tcagggtgcc tgagttgcca gaactggagc cagaaaatct gtcagggacc 660
 cctgagggtc gatccccatc actgtccacg aggactgtag gggcctttcc tgggagttgt 720
 tgggtaccagt tcacaccgaa tatatcaatg tcattcgtgt ctccagagca ggagatggtg 780
 accttctggc ccaggggccc agatactgag gccggctgat tcaacacagc ctgggcccag 840
 gaccctgtgc agtgagcgag gagtgtgagg aggagagggg accaggccat gtcggaggac 900
 atcactgatt gatcctgcct tctggggacc ctcgtgcc 938

<210> 28
 <211> 578
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(423)
 <223>

<220>

<221> misc_feature
 <222> (471)..(471)
 <223> At nucleotide 471, n = unknown

<220>
 <221> misc_feature
 <222> (481)..(481)
 <223> At nucleotide 481, n = unknown

<220>
 <221> misc_feature
 <222> (522)..(522)
 <223> At nucleotide 522, n = unknown

<220>
 <221> misc_feature
 <222> (549)..(549)
 <223> At nucleotide 549, n = unknown

<400> 28
 cat caa gat tgg ttt aat ggt aag gag ttc aaa tgt aga gtc aac cac 48
 His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His
 1 5 10 15
 ata gac ctc ccg tct ccc atc gag agg acc atc tct aag gcc aga ggg 96
 Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
 20 25 30
 agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca tcc cca aag gag 144
 Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
 35 40 45
 ttg tca tcc agt gac aca gtc agc atc acc tgc ctg ata aaa gac ttc 192
 Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
 50 55 60
 tac cca cct gac att gat gtg gag tgg cag agc aat gga cag cag gag 240
 Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
 65 70 75 80
 cct gag agc aag tac cgc acg acc ccg ccc cag ctg gac gag gac ggg 288
 Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
 85 90 95
 tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc cgc tgg cag 336
 Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
 100 105 110
 cgg gga gac acc ttc ata tgt gcg gtg atg cat gaa gct cta cac aac 384
 Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
 115 120 125
 cac tac aca cag aaa tcc ctc tcc cat tct ccg ggt aaa tgagcaacac 433

His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys
130 135 140

gcccggcacc cagcaagccc cccacccttg gctctcanga tccctganga cacctgagcc 493
cctgtccctg tgtacataac cctgggtang cacccatcat gaaataaagc acccancact 553
gccctgggccc cttgcaaaaa aaaaa 578

<210> 29
<211> 141
<212> PRT
<213> Canis familiaris

<400> 29

His Gln Asp Trp Phe Asn Gly Lys Glu Phe Lys Cys Arg Val Asn His
1 5 10 15

Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly
20 25 30

Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro Ser Pro Lys Glu
35 40 45

Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu Ile Lys Asp Phe
50 55 60

Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn Gly Gln Gln Glu
65 70 75 80

Pro Glu Ser Lys Tyr Arg Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly
85 90 95

Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser Arg Trp Gln
100 105 110

Arg Gly Asp Thr Phe Ile Cys Ala Val Met His Glu Ala Leu His Asn
115 120 125

His Tyr Thr Gln Lys Ser Leu Ser His Ser Pro Gly Lys
130 135 140

<210> 30
<211> 578
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (30)..(30)
<223> At nucleotide 30, n = unknown

<220>
<221> misc_feature
<222> (57)..(57)
<223> At nucleotide 57, n = unknown

<220>
<221> misc_feature
<222> (98)..(98)
<223> At nucleotide 98, n = unknown

<220>
<221> misc_feature
<222> (108)..(108)
<223> At nucleotide 108, n = unknown

<400> 30
tttttttttt gcaagggccc agggcagtg tgggtgcttt atttcatgat ggggtgcntac 60
ccaggggttat gtacacaggg acaggggctc aggtgtcntc agggatcntg agagccaagg 120
gtgggggggct tgctgggtgc cgggcgtggt gctcatttac ccggagaatg ggagagggat 180
ttctgtgtgt agtggttgtg tagagcttca tgcatacccg cacatatgaa ggtgtctccc 240
cgctgccagc ggctcttgtc cacagagagc ttgctgtaca ggaagtagga cccgtcctcg 300
tccagctggg gcggggtcgt gcggtacttg ctctcaggct cctgctgtcc attgctctgc 360
cactccacat caatgtcagg tgggtagaag tcttttatca ggcaggtgat gctgactgtg 420
tactggatg acaactcctt tggggatggc ggcaggacat acacactggg cttatgggcc 480
ctccctctgg ccttagagat ggtcctctcg atgggagacg ggaggtctat gtggttgact 540
ctacatttga actccttacc attaaaccaa tcttgatg 578

<210> 31
<211> 1364
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (59)..(1183)
<223>

<400> 31
ggcagcaggc cgattcacca tttccagaga caatgtcgag aacacgctgt atctgcag 58

atg aac agc ctg aga gct gag gat acg gcc ctg tat tac tgt aca agt 106
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser
1 5 10 15

ggg tta tgg atc aac tgg tac ggt ccg aat ttt gac tcc tgg ggc cag 154
Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln
20 25 30

gga acc ctg gtc acc gtc tcc tca gcc tcc acc acg gcc ccc tcg gtt 202
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
35 40 45

ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc 250
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
50 55 60

ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc 298
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
65 70 75 80

tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc 346
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
85 90 95

ctg cag tcc tca ggg ctc tac tcc ctc agc agc atg gtg aca gtg ccc 394
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro
100 105 110

tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gcc cac ccg 442
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro
115 120 125

gcc agc aaa act aaa gta gac aag cca gtg ccc aaa aga gaa aat gga 490
Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly
130 135 140

aga gtt cct cgc cca cct gat tgt ccc aaa tgc cca acc cct gaa atg 538
Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Thr Pro Glu Met
145 150 155 160

ctg gga ggg cct tcg gtc ttc atc ttt ccc ccg aaa ccc aag gac acc 586
Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr
165 170 175

ctc ttg att gcc cga aca cct gag gtc aca tgt gtg gtg gtg gat ctg 634
Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu
180 185 190

gac cca gaa gac cct gag gtg cag atc agc tgg ttc gtg gac ggt aag 682
Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys
195 200 205

cag atg caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc 730

Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly	
210 215 220	
acc tac cgt gtg gtc agt gtc ctc ccc att ggg cac cag gac tgg ctc	778
Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu	
225 230 235 240	
aag ggg aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctc cca tcc	826
Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser	
245 250 255	
cca atc gag agg acc atc tcc aag gcc aga ggg cag gcc cat caa ccc	874
Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro	
260 265 270	
agt gtg tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca	922
Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr	
275 280 285	
gtc agc ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat	970
Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp	
290 295 300	
gtg gag tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc	1018
Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg	
305 310 315 320	
acg acc ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc	1066
Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser	
325 330 335	
aag ctc tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata	1114
Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile	
340 345 350	
tgt gcg gtg atg cat gaa gct tta cac aac cac tac aca cag aaa tcc	1162
Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser	
355 360 365	
ctc tcc cat tct ccg ggt aaa tgagcaacac gcccggcacc cagcaagccc	1213
Leu Ser His Ser Pro Gly Lys	
370 375	
cccacccttg gctttcagga tcccatgagg atgcctgagc ccccatccct gtgtacataa	1273
ccccgggtag gcacctggca tgaaataaag caccagtagc tgccctggaa aaaaaaaaaa	1333
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a	1364

<210> 32
 <211> 375
 <212> PRT
 <213> Canis familiaris .
 <400> 32

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys Thr Ser
1 5 10 15

Gly Leu Trp Ile Asn Trp Tyr Gly Pro Asn Phe Asp Ser Trp Gly Gln
20 25 30

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val
35 40 45

Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala
50 55 60

Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser
65 70 75 80

Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val
85 90 95

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Met Val Thr Val Pro
100 105 110

Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Ala His Pro
115 120 125

Ala Ser Lys Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly
130 135 140

Arg Val Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Thr Pro Glu Met
145 150 155 160

Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr
165 170 175

Leu Leu Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu
180 185 190

Asp Pro Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys
195 200 205

Gln Met Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly
210 215 220

Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu

225 230 235 240

Lys Gly Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser
245 250 255

Pro Ile Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro
260 265 270

Ser Val Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr
275 280 285

Val Ser Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp
290 295 300

Val Glu Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg
305 310 315 320

Thr Thr Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser
325 330 335

Lys Leu Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile
340 345 350

Cys Ala Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
355 360 365

Leu Ser His Ser Pro Gly Lys
370 375

<210> 33
<211> 1364
<212> DNA
<213> Canis familiaris

<400> 33
 tttttttttt tttttttttt tttttttttt tttttttttt tttccagggc agtactgggt 60
 gctttatttc atgccaggtg cctaccggg gttatgtaca cagggatggg ggctcaggca 120
 tcctcatggg atcctgaaag ccaaggggtg ggggcttgct gggtgccggg cgtgttgctc 180
 atttaccggg agaatgggag agggatttct gtgtgtagtg gttgtgtaaa gcttcatgca 240
 tcaccgcaca tatgaaggtg tctccccgct gccagcggct cttgtccaca gagagcttgc 300
 tgtacaggaa gtaggacctg tctcgtcca gctggggcgg ggtcgtgcgg tacttgctct 360

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caggctcctg ctgtccattg ctctgccact ccacatcaat gtcagggtggg aagaagtctt 420
tgatcaggca tgtcaagctg actgtgttct tgctcaactc ctcccgggat ggcggcagga 480
catacacact gggttgatgg gcctgccctc tggccttgga gatggtcctc tcgattgggg 540
atgggagggc tttgttggtg actttgcacg tgaactgctt ccccttgagc cagtcttggt 600
gcccaatggg gaggacactg accacacggg aggtgccatt gaactgctcc tcacgaggct 660
gagtcttggc tgtttgcacg tgcttaccgt ccacgaacca gctgatctgc acctcagggt 720
cttctgggtc cagatccacc accacacatg tgacctcagg tgttcgggca atcaagaggg 780
tgtccttggg tttcggggga aagatgaaga ccgaaggccc tcccagcatt tcaggggttg 840
ggcatttggg acaatcaggg gggcgaggaa ctcttccatt ttctcttttg ggcactggct 900
tgtctacttt agttttgctg gccgggtggg ccacgttgca ggtgaaggct tcgctggggc 960
acctgctgga gggcactgtc accatgctgc tgagggagta gagccctgag gactgcagga 1020
cggacgggaa ggtgtgcaca ccgctggtca aggagccgga attccaggac acagttacag 1080
gctcggggaa gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc 1140
cgcagctggg ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gagacggtga 1200
ccagggttcc ctggccccag gagtcaaaat tcggaccgta ccagttgatc cataaccac 1260
ttgtacagta atacagggcc gtatcctcag ctctcaggct gttcatctgc agatacagcg 1320
tgttctcgac attgtctctg gaaatggtga atcggcctcg tgcc 1364

```

```

<210> 34
<211> 1168
<212> DNA
<213> Canis familiaris

```

```

<220>
<221> CDS
<222> (48) .. (1166)
<223>

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<400> 34
ccagggtgacc ccattcagtg ctcaggacac aacacagaca aaccacc atg gag tct 56
                                         Met Glu Ser
                                         1

gtg ctc tgc tgg gtt ttc ctt gtc tct att tta aaa ggt gtc cag ggt 104
Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly Val Gln Gly
      5                10                15

gag gtg caa ctg gtg gag tct ggg gga gac ctg gtg aag cct ggg ggg 152
Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly

```

20					25					30					35	
tcc ttg aga ctg tcc tgt gtg gcc tct gga ttc acc ttc agt gac tat	200															
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asp Tyr																
				40					45					50		
ggc atg agt tgg gtc cgt cag tct cca ggg aag ggg ctg cag tgg gtc	248															
Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Gln Trp Val																
			55					60					65			
gca gct gtt agc aat cgt gga gat act tac tac gca gac gct gtg aag	296															
Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp Ala Val Lys																
		70					75					80				
ggc cga ttc acc atc tcc aga gac aac gcc aag aac acg ctg tat ctc	344															
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu																
	85					90				95						
cag atg agc agc ctg aaa gcc gag gac acg gca atc tat cac tgt gtg	392															
Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr His Cys Val																
100					105				110						115	
acg gga gta tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat	440															
Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn																
			120					125					130			
ggc acc tca ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt	488															
Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val																
			135					140					145			
ttc cca ctg gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc	536															
Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala																
		150					155					160				
ctg gcc tgc ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc	584															
Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser																
	165					170				175						
tgg aat tcc ggc tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc	632															
Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val																
180					185				190						195	
ctg cag tcc tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc	680															
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro																
			200					205					210			
tcc agc agg tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg	728															
Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro																
			215					220					225			
gcc agc aac act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc	776															
Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys																
		230					235					240				
aag tgt ata tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg	824															
Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser																
	245					250				255						

gtc ttc atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga	872
Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg	
260 265 270 275	
aca ccc gag atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct	920
Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro	
280 285 290	
gag gtg cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc	968
Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala	
295 300 305	
aag acg cag cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc	1016
Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val	
310 315 320	
agc gtc ctc ccc att gag cac cag gac tgg ctc acc gga aag gag ttc	1064
Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe	
325 330 335	
aag tgc aga gtc aac cac ata ggc ccc ccg tcc ccc atc gag agg act	1112
Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile Glu Arg Thr	
340 345 350 355	
atc tcc aaa gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg	1160
Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu	
360 365 370	
ccg cca tc	1168
Pro Pro	

<210> 35
 <211> 373
 <212> PRT
 <213> Canis familiaris

<400> 35

Met Glu Ser Val Leu Cys Trp Val Phe Leu Val Ser Ile Leu Lys Gly
1 5 10 15
Val Gln Gly Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys
20 25 30
Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe
35 40 45
Ser Asp Tyr Gly Met Ser Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
50 55 60

Gln Trp Val Ala Ala Val Ser Asn Arg Gly Asp Thr Tyr Tyr Ala Asp
65 70 75 80

Ala Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Met Ser Ser Leu Lys Ala Glu Asp Thr Ala Ile Tyr
100 105 110

His Cys Val Thr Gly Val Trp Pro Arg His Tyr Tyr Gly Met Asp His
115 120 125

Trp Gly Asn Gly Thr Ser Leu Phe Val Ser Ser Ala Ser Thr Thr Ala
130 135 140

Pro Ser Val Phe Pro Leu Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser
145 150 155 160

Thr Val Ala Leu Ala Cys Leu Val Ser Gly Tyr Phe Pro Glu Pro Val
165 170 175

Thr Val Ser Trp Asn Ser Gly Ser Leu Thr Ser Gly Val His Thr Phe
180 185 190

Pro Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val
195 200 205

Thr Val Pro Ser Ser Arg Trp Pro Ser Glu Thr Phe Thr Cys Asn Val
210 215 220

Val His Pro Ala Ser Asn Thr Lys Val Asp Lys Pro Val Pro Lys Glu
225 230 235 240

Ser Thr Cys Lys Cys Ile Ser Pro Cys Pro Val Pro Glu Ser Leu Gly
245 250 255

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg
260 265 270

Ile Thr Arg Thr Pro Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg
275 280 285

Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val

290		295		300
His Thr Ala Lys Thr Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr				
305		310		315 320
Arg Val Val Ser Val Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly				
	325		330	335
Lys Glu Phe Lys Cys Arg Val Asn His Ile Gly Pro Pro Ser Pro Ile				
	340		345	350
Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val				
	355		360	365
Tyr Val Leu Pro Pro				
370				

<210> 36
 <211> 1168
 <212> DNA
 <213> Canis familiaris

<400> 36	
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ctctcgatgg gggacggggg gcctatgtgg ttgactctgc acttgaactc ctttcgggtg	120
agccagtcct ggtgctcaat ggggaggacg ctgaccacac ggtaggtgct gttgaactgc	180
tgctcacgag gctgcgtctt ggctgtgtgc acctccttac catccacgaa ccagctgac	240
tgcacctcag ggtcctcag gccagatct aacaccacac aggtgatctc ggggtgttcgg	300
gtaatcctga ggatgtcctt gggtttcggg ggaaagatga agaccgaagg ccctcccagt	360
gattcagga ctgggcatgg ggatatacac ttgcaggtgg actctttggg cactggcttg	420
tctactttag tgttgctggc cgggtggacc acgttgacg tgaaggtctc gctgggccac	480
ctgctggagg gactgtcac cgtgctgctg agggagtaga gccctgagga ctgcaggacg	540
gacgggaagg tgtgcacacc gctggtcaag gagccggaat tccaggacac agttacaggc	600
tcgggggaagt agcctgacac caggcaggcc agggccaccg tggagccgga agtggaccgc	660
cagctggggg ccagtgggaa aaccgagggg gccgtggtgg aggctgagga cacgaagagt	720
gaggtgccat tgccccagtg gtccatacca taataatgtc gcggccatac tcccgtcaca	780
cagtgataga ttgccgtgtc ctcggttttc aggtgctca tctggagata cagcgtgttc	840

ttggcgttgt ctctggagat ggtgaatcgg cccttcacag cgtctgcgta gtaagtatct 900
ccacgattgc taacagctgc gaccactgc agccccctcc ctggagactg acggacccaa 960
ctcatgccat agtcactgaa ggtgaatcca gaggccacac aggacagtct caaggacccc 1020
ccaggcttca ccaggtctcc cccagactcc accagttgca cctcaccctg gacacctttt 1080
aaaatagaga caaggaaaac ccagcagagc acagactcca tgggtggttg tctgtgttgt 1140
gtcctgagca ctgaatgggg tcacctgg 1168

<210> 37
<211> 1059
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1056)
<223>

<400> 37
tgg ccg cga cat tat tat ggt atg gac cac tgg ggc aat ggc acc tca 48
Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser
1 5 10 15
ctc ttc gtg tcc tca gcc tcc acc acg gcc ccc tcg gtt ttc cca ctg 96
Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu
20 25 30
gcc ccc agc tgc ggg tcc act tcc ggc tcc acg gtg gcc ctg gcc tgc 144
Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys
35 40 45
ctg gtg tca ggc tac ttc ccc gag cct gta act gtg tcc tgg aat tcc 192
Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
50 55 60
gac tcc ttg acc agc ggt gtg cac acc ttc ccg tcc gtc ctg cag tcc 240
Asp Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser
65 70 75 80
tca ggg ctc tac tcc ctc agc agc acg gtg aca gtg ccc tcc agc agg 288
Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg
85 90 95
tgg ccc agc gag acc ttc acc tgc aac gtg gtc cac ccg gcc agc aac 336
Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn
100 105 110
act aaa gta gac aag cca gtg ccc aaa gag tcc acc tgc aag tgt ata 384
Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile
115 120 125

tcc cca tgc cca gtc cct gaa tca ctg gga ggg cct tcg gtc ttc atc	432
Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile	
130 135 140	
ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc gag	480
Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu	
145 150 155 160	
atc acc tgt gtg gtg tta gat ctg ggc cgt gag gac cct gag gtg cag	528
Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln	
165 170 175	
atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acg cag	576
Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln	
180 185 190	
cct cgt gag cag cag ttc aac agc acc tac cgt gtg gtc agc gtc ctc	624
Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu	
195 200 205	
ccc att gag cac cag gac tgg ctc acc gga aag gag ttc aag tgc aga	672
Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg	
210 215 220	
gtc aac cac ata ggc ctc ccg tcc ccc atc gag agg act atc tcc aaa	720
Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys	
225 230 235 240	
gcc aga ggg caa gcc cat cag ccc agt gtg tat gtc ctg cca cca tcc	768
Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser	
245 250 255	
cca aag gag ttg tca tcc agt gac acg gtc acc ctg acc tgc ctg atc	816
Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile	
260 265 270	
aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag agc aat gga	864
Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly	
275 280 285	
cag ccg gag ccc gag agc aag tac cac acg act gcg ccc cag ctg gac	912
Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp	
290 295 300	
gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag agc	960
Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser	
305 310 315 320	
cgc tgg cag cag gga gac ccc ttc aca tgt gcg gtg atg cat gaa gct	1008
Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala	
325 330 335	
cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt aaa	1056
Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys	
340 345 350	
tga	1059

<210> 38
 <211> 352
 <212> PRT
 <213> Canis familiaris

<400> 38

Trp Pro Arg His Tyr Tyr Gly Met Asp His Trp Gly Asn Gly Thr Ser
 1 5 10 15

Leu Phe Val Ser Ser Ala Ser Thr Thr Ala Pro Ser Val Phe Pro Leu
 20 25 30

Ala Pro Ser Cys Gly Ser Thr Ser Gly Ser Thr Val Ala Leu Ala Cys
 35 40 45

Leu Val Ser Gly Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 50 55 60

Asp Ser Leu Thr Ser Gly Val His Thr Phe Pro Ser Val Leu Gln Ser
 65 70 75 80

Ser Gly Leu Tyr Ser Leu Ser Ser Thr Val Thr Val Pro Ser Ser Arg
 85 90 95

Trp Pro Ser Glu Thr Phe Thr Cys Asn Val Val His Pro Ala Ser Asn
 100 105 110

Thr Lys Val Asp Lys Pro Val Pro Lys Glu Ser Thr Cys Lys Cys Ile
 115 120 125

Ser Pro Cys Pro Val Pro Glu Ser Leu Gly Gly Pro Ser Val Phe Ile
 130 135 140

Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro Glu
 145 150 155 160

Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val Gln
 165 170 175

Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr Gln
 180 185 190

Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
195 200 205

Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Arg
210 215 220

Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser Lys
225 230 235 240

Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro Ser
245 250 255

Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu Ile
260 265 270

Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn Gly
275 280 285

Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu Asp
290 295 300

Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys Ser
305 310 315 320

Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu Ala
325 330 335

Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly Lys
340 345 350

<210> 39
<211> 1059
<212> DNA
<213> Canis familiaris

<400> 39
tcatttaccc ggagaatggg agagggatag atctgtgtag tggttctgta gagcttcattg 60
catcaccgca catgtgaagg ggtctccctg ctgccagcgg ctcttggtcca cagagagctt 120
gctgtacagg aagtaggacc cgtcctcgtc cagctggggc gcagtcgtgt ggtacttgct 180
ctcgggctcc ggctgtccat tgctctgcca ctccacatca atctcaggtg ggaagaagtc 240
tttgatcagg caggtcaggg tgaccgtgtc actggatgac aactcctttg gggatgggtg 300
caggacatac aactgggct gatgggcttg ccctctggct ttggagatag tcctctcgat 360

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gggggacggg aggcctatgt ggttgactct gcacttgaac tcctttccgg tgagccagtc 420
ctgggtgctca atggggagga cgctgaccac acggtaggtg ctggtgaact gctgctcacg 480
aggctgcgtc ttggctgtgt gcacctcctt accatccacg aaccagctga tctgcacctc 540
agggtcctca cggcccagat ctaacaccac acaggtgatc tcgggtgttc gggtaatcct 600
gaggatgtcc ttgggtttcg ggggaaagat gaagaccgaa ggccctccca gtgattcagg 660
gactgggcat ggggatatac acttgacagt ggactctttg ggcactggct tgtctacttt 720
agtgttgctg gccgggtgga ccacgttgca ggtgaaggtc tcgctgggcc acctgctgga 780
gggcactgtc accgtgctgc tgaggagagta gagccctgag gactgcagga cggacgggaa 840
ggtgtgcaca ccgctgggtc aggagtcgga attccaggac acagttacag gctcggggaa 900
gtagcctgac accaggcagg ccagggccac cgtggagccg gaagtggacc cgcagctggg 960
ggccagtggg aaaaccgagg gggccgtggt ggaggctgag gacacgaaga gtgaggtgcc 1020
attgccccag tgggtccatac cataataatg tcgcggcc 1059

```

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<210> 40
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<220>
<221> misc_feature
<222> (15)..(15)
<223> At nucleotide 15, n = unknown

```

```

<220>
<221> misc_feature
<222> (21)..(21)
<223> At nucleotide 21, n = unknown

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```

<400> 40
caycargayt ggytnaaygg naargartty aartgy 36

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```

<210> 41
<211> 28
<212> DNA
<213> Artificial sequence

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```

<220>
<223> Synthetic Primer

```


<400> 41
gccctccagc aggtggccca gcgagacc 28

<210> 42
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 42
ggggatggcg gcaggacata cac 23

<210> 43
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 43
tttaccgga gaatgggaga ggg 23

<210> 44
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 44
ggtctgcgtg ggccacctgc tggagggc 28

<210> 45
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 45
gggtgggggg cttgctgggt gccgggcg 28

<210> 46
<211> 30
<212> DNA
<213> Artificial sequence

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<220>
<223> Synthetic Primer

<400> 46
ccaggtgacc ccattcagtg ctcaggacac 30

<210> 47
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 47
ctgtgtgacg ggagtatggc cgcgac 26

<210> 48
<211> 483
<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (470)..(470)
<223> At nucleotide 470, n = unknown

<400> 48
cttatttgga catggaaccc cccagagggc gccagcccga attgcacctt acggtatttt 60
agtcattttg acaacaaaca ggataagaaa attgctcctg aaactcatcg ttcaaaagaa 120
gtacccttga atgagaggat ttgtctgcaa gtgggggtccc agtgcagcac caatgaaagt 180
gacaatccta gcatttttggg ggaaaagtgc accccaccac ctgaaggtgg tcttgagtcg 240
gctgtgactg agctacaatg tgtttggcac aacctgagct acatgaagtg tacttggctt 300
cctggaagga atacaagccc tgacaccaac tatactctct actattggca cagcagcctg 360
ggaaaaattc ttcaatgcga agacatctat agagaaggtc aacacattgg ttgttccttt 420
gctctgacta atttgaagga ttccagtttt gaacaacaca gtgtccagan gatgggtcaag 480
ggt 483

<210> 49
<211> 1547
<212> DNA
<213> Canis familiaris

<220>

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<221> CDS
 <222> (1)..(1215)
 <223>

<400> 49

ggc ggg gtc gcc gca ccc acc gaa act cag cca cct gtg acg aat ttg	48
Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu	
1 5 10 15	
agt gtt tct gtt gaa aac ctc tgc acg gtc ata tgg aca tgg aac cct	96
Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro	
20 25 30	
ccc gag gga gcc agc ccg aat tgc acc tta cgg tat ttt agt cat ttt	144
Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe	
35 40 45	
gac aac aaa cag gat aag aaa att gct cct gaa act cat cgt tca aaa	192
Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys	
50 55 60	
gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag tgc	240
Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys	
65 70 75 80	
agc acc aat gaa agt gac aat cct agc att ttg gtg gaa aag tgc acc	288
Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr	
85 90 95	
cca cca cct gaa ggt gat cct gag tcg gct gtg act gag cta caa tgt	336
Pro Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys	
100 105 110	
gtt tgg cac aac ctg agc tac atg aag tgt act ttg ctt cct gga agg	384
Val Trp His Asn Leu Ser Tyr Met Lys Cys Thr Trp Leu Pro Gly Arg	
115 120 125	
aat aca agc cct gac acc aac tat act ctc tac tat tgg cac agc agc	432
Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Trp Trp His Ser Ser	
130 135 140	
ctg gga aaa att ctt caa tgc gaa gac atc tat aga gaa ggt caa cac	480
Leu Gly Lys Ile Leu Gln Cys Glu Asp Ile Tyr Arg Glu Gly Gln His	
145 150 155 160	
att ggt tgt tcc ttt gct ctg act aat ttg aag gat tcc agt ttt gaa	528
Ile Gly Cys Ser Phe Ala Leu Thr Asn Leu Lys Asp Ser Ser Phe Glu	
165 170 175	
caa cac agt gtc caa ata atg gtc aag gat aat gca aga aaa att aga	576
Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Arg Lys Ile Arg	
180 185 190	
ccg tcc ttc aat ata gtg cct tta act tct cat gtg aaa cct gat ccc	624
Pro Ser Phe Asn Ile Val Pro Leu Thr Ser His Val Lys Pro Asp Pro	
195 200 205	

ccc cat att aag cgt ctc ttc ttc caa aat ggt aac ttg tat gtg caa	672
Pro His Ile Lys Arg Leu Phe Phe Gln Asn Gly Asn Leu Tyr Val Gln	
210 215 220	
tgg aag aat cca caa aat ttt tat agc aga tgc tta tct tac caa gta	720
Trp Lys Asn Pro Gln Asn Phe Tyr Ser Arg Cys Leu Ser Tyr Gln Val	
225 230 235 240	
gaa gtc aat aac agc cag act gag acg aat gat ata ttc tac gtt gaa	768
Glu Val Asn Asn Ser Gln Thr Glu Thr Asn Asp Ile Phe Tyr Val Glu	
245 250 255	
gaa gcc aaa tgt cag aat tca gaa ttt gag gga aac ctg gag ggt aca	816
Glu Ala Lys Cys Gln Asn Ser Glu Phe Glu Gly Asn Leu Glu Gly Thr	
260 265 270	
att tgt ttc atg gtc ccc ggc gtt ctt cct gat act ttg aac aca gtc	864
Ile Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr Val	
275 280 285	
aga ata aga gtc aga aca aat aag tta tgc tat gag gat gac aaa ctc	912
Arg Ile Arg Val Arg Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys Leu	
290 295 300	
tgg agt aat tgg agt caa gcg atg agt ata ggt gag aat acc gac ccc	960
Trp Ser Asn Trp Ser Gln Ala Met Ser Ile Gly Glu Asn Thr Asp Pro	
305 310 315 320	
acg ttc tat ata acc atg ttg ctc gcc act caa gtc atc gtt gca ggt	1008
Thr Phe Tyr Ile Thr Met Leu Leu Ala Thr Gln Val Ile Val Ala Gly	
325 330 335	
gcc atc ata atc ctt ctg ctt tat ctc aaa agg ctc aag atc att ata	1056
Ala Ile Ile Ile Leu Leu Leu Tyr Leu Lys Arg Leu Lys Ile Ile Ile	
340 345 350	
ttc cct cca att cct gat cct ggc aag att ttt aaa gaa atg ttt gga	1104
Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly	
355 360 365	
gac cag aat gat gat acg ctg cac tgg agg aag tac gac atc tat gag	1152
Asp Gln Asn Asp Asp Thr Leu His Trp Arg Lys Tyr Asp Ile Tyr Glu	
370 375 380	
aag caa aca aaa gaa gaa acg gac tca gta gtg ctg att gaa aac ctg	1200
Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val Leu Ile Glu Asn Leu	
385 390 395 400	
aag aaa gcc tct cag taatggggat aacttatttt agccttcagc atgaccttgt	1255
Lys Lys Ala Ser Gln	
405	
aaagattcat cccacgttc tcgggaagct tcaagggtcaa gcatcttggg aaaggacatt	1315
acagtttcta cagcatgggtg tacctgggca tctccgacta cttcttcaac acagcagggc	1375

ttgtgtacca agaggcaggg gccttaaaca tgaccatcac ggacgacatg ataccaaaga 1435

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<210> 50

<211> 405

<212> PRT

<213> Canis familiaris

<400> 50

Gly Gly Val Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn Leu
1 5 10 15

Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn Pro
20 25 30

Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr Phe Ser His Phe
35 40 45

Asp Asn Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr His Arg Ser Lys
50 55 60

Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln Cys
65 70 75 80

Ser Thr Asn Glu Ser Asp Asn Pro Ser Ile Leu Val Glu Lys Cys Thr
85 90 95

Pro Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln Cys
100 105 110

Val Trp His Asn Leu Ser Tyr Met Lys Cys Thr Trp Leu Pro Gly Arg
115 120 125

Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Ser Ser
130 135 140

Leu Gly Lys Ile Leu Gln Cys Glu Asp Ile Tyr Arg Glu Gly Gln His
145 150 155 160

Ile Gly Cys Ser Phe Ala Leu Thr Asn Leu Lys Asp Ser Ser Phe Glu
165 170 175

Gln	His	Ser	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Arg	Lys	Ile	Arg	180	185	190
Pro	Ser	Phe	Asn	Ile	Val	Pro	Leu	Thr	Ser	His	Val	Lys	Pro	Asp	Pro	195	200	205
Pro	His	Ile	Lys	Arg	Leu	Phe	Phe	Gln	Asn	Gly	Asn	Leu	Tyr	Val	Gln	210	215	220
Trp	Lys	Asn	Pro	Gln	Asn	Phe	Tyr	Ser	Arg	Cys	Leu	Ser	Tyr	Gln	Val	225	230	235
Glu	Val	Asn	Asn	Ser	Gln	Thr	Glu	Thr	Asn	Asp	Ile	Phe	Tyr	Val	Glu	245	250	255
Glu	Ala	Lys	Cys	Gln	Asn	Ser	Glu	Phe	Glu	Gly	Asn	Leu	Glu	Gly	Thr	260	265	270
Ile	Cys	Phe	Met	Val	Pro	Gly	Val	Leu	Pro	Asp	Thr	Leu	Asn	Thr	Val	275	280	285
Arg	Ile	Arg	Val	Arg	Thr	Asn	Lys	Leu	Cys	Tyr	Glu	Asp	Asp	Lys	Leu	290	295	300
Trp	Ser	Asn	Trp	Ser	Gln	Ala	Met	Ser	Ile	Gly	Glu	Asn	Thr	Asp	Pro	305	310	315
Thr	Phe	Tyr	Ile	Thr	Met	Leu	Leu	Ala	Thr	Gln	Val	Ile	Val	Ala	Gly	325	330	335
Ala	Ile	Ile	Ile	Leu	Leu	Leu	Tyr	Leu	Lys	Arg	Leu	Lys	Ile	Ile	Ile	340	345	350
Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile	Phe	Lys	Glu	Met	Phe	Gly	355	360	365
Asp	Gln	Asn	Asp	Asp	Thr	Leu	His	Trp	Arg	Lys	Tyr	Asp	Ile	Tyr	Glu	370	375	380
Lys	Gln	Thr	Lys	Glu	Glu	Thr	Asp	Ser	Val	Val	Leu	Ile	Glu	Asn	Leu	385	390	395
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Lys Lys Ala Ser Gln
405

<210> 51
<211> 1547
<212> DNA
<213> Canis familiaris

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atcatgtcgt ccgatgatggg catgttttaag gccctgcct cttggtacac aagccctgct 180
gtgttgaaga agtagtcgga gatgccaggg tacaccatgc tgtagaaact gtaatgtcct 240
ttcccaagat gcttgacctt gaagcttccc gagaacgtgg ggatgaatct ttacaaggtc 300
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agcactactg agtccgtttc ttcttttgtt tgcttctcat agatgtcgta cttcctccag 420
tgcagcgtat catcattctg gtctccaaac atttctttaa aaatcttgcc aggatcagga 480
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tcaacgtaga atatatcatt cgtctcagtc tggctgttat tgacttctac ttggtaagat 840
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<210> 52
<211> 1215
<212> DNA
<213> *Canis familiaris*

<400> 52
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accttacggt attttagtca ttttgacaac aacaggata agaaaattgc tcctgaaact 180
catcgttcaa aagaagtacc cctgaatgag aggatttgct tgcaagtggg gtcccagtgc 240
agcaccaatg aaagtgacaa tcctagcatt ttggtggaaa agtgcacccc accacctgaa 300
ggtgatcctg agtcggctgt gactgagcta caatgtgttt ggcacaacct gagctacatg 360
aagtgtactt ggcttcctgg aaggaataca agccctgaca ccaactatac tctctactat 420
tggcacagca gcctgggaaa aattcttcaa tgcaagaca tctatagaga aggtcaacac 480
attggttggt cctttgctct gactaatttg aaggattcca gttttgaaca acacagtgtc 540
caaataatgg tcaaggataa tgcaagaaaa attagaccgt cttcaatat agtgccttta 600
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ttgtatgtgc aatggaagaa tccacaaaat ttttatagca gatgcttata ttaccaagta 720
gaagtcaata acagccagac tgagacgaat gatataattct acgttgaaga agccaaatgt 780
cagaattcag aatttgaggg aaacctggag ggtacaattt gtttcatggt cccggcggtt 840
cttctgata ctttgaacac agtcagaata agagtcagaa caaataagtt atgctatgag 900
gatgacaaac tctggagtaa ttggagtcaa gcgatgagta taggtgagaa taccgacccc 960
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cttctgcttt atctcaaaag gctcaagatc attatattcc ctccaattcc tgatcctggc 1080
aagattttta aagaaatggt tggagaccag aatgatgata cgctgcactg gaggaagtac 1140
gacatctatg agaagcaaac aaaagaagaa acggactcag tagtgctgat tgaaaacctg 1200
aagaaagcct ctcatg 1215

<210> 53
<211> 1215

<212> DNA

<213> Canis familiaris

<400> 53

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ttcttttaaaa atcttgccag gatcaggaat tggagggaat ataatgatct tgagcctttt      180
gagataaagc agaaggatta tgatggcacc tgcaacgatg acttgagtgg cgagcaacat      240
ggttatatag aacgtggggg cggtattctc acctatactc atcgcttgac tccaattact      300
ccagagtttg tcctcctcat agcataactt atttgttctg actcttattc tgactgtggt      360
caaagtatca ggaagaacgc cggggacat gaaacaaatt gtaccctcca gggttccctc      420
aaattctgaa ttctgacatt tggcttcttc aacgtagaat atatcattcg tctcagtcgt      480
gctgttattg acttctactt ggtaagataa gcatctgcta taaaaatttt gtggattctt      540
ccattgcaca tacaagttac ctttttgaa gaagagacgc ttaatatggg ggggatcagg      600
ttcacatga gaagttaaag gcactatatt gaaggacggg ctaatttttc ttgcattatc      660
cttgaccatt atttgacac tgtgttggtc aaaactggaa tccttcaaat tagtcagagc      720
aaaggaacaa ccaatgtggt gaccttctct atagatgtct tcgcattgaa gaatttttcc      780
caggctgctg tgccaatagt agagagtata gttgggtgtca gggcttgat tccttcagg      840
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actttcattg gtgctgcact gggacccac ttgcagacaa atcctctcat tcaggggtac     1020
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aaaataccgt aaggtgcaat tcgggctggc tcctcggga gggttccatg tccatatgac     1140
cgtgcagagg ttttcaacag aaacactcaa attcgtcaca ggtggctgag tttcggtgagg     1200
tgcggcgacc ccgcc                                           1215

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<210> 54

<211> 620

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (184)..(618)

<223>

<400> 54
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aattaatgtc tccaaactgg agaagagaaa aaaaagagga cctgtgataa ttgcctatga 120
taattcattt cttgagaaac catattattg agtggaact tcaaagtatt gaatcttgga 180
gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt 228
Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
1 5 10 15
gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt 276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
20 25 30
aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat 324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45
ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa 372
Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu
50 55 60
tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac 420
Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn
65 70 75
tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat 468
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
80 85 90 95
ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa 516
Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln
100 105 110
tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat 564
Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125
tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac 612
Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp
130 135 140
tgt gta ta 620
Cys Val
145

<210> 55
<211> 145
<212> PRT
<213> Canis familiaris

<400> 55

Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu Val

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Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn	20	25	30
Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu	35	40	45
Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys	50	55	60
Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp	65	70	75
Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu	85	90	95
Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys	100	105	110
Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp	115	120	125
Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys	130	135	140

Val
145

<210> 56
<211> 620
<212> DNA
<213> Canis familiaris

<400> 56	
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gtgtttatct ttgcttcaat acctttgtta agatcaaacc catcttttgta atgtagattc	180
ttggtaatga tgggtcttcca gttttcacta tcaatgtttc ggtatttttaa ttcatatctt	240
attgtgcatt ccttaaaatt atccggaaat aatggagggt gccattgcaa agagagataa	300
cctaaatatt caggggtccac tatctcaaaa tcttgaggag gattaacttt tatctcagca	360

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tttgaagca tagagccaaa tgctgtgcaa acaagcaggg tatagaggaa tccgacatcc 420
aatgaatga aagccattcc tccaagattc aatactttga agtttccact caataatatg 480
gtttctcaag aaatgaatta tcataggcaa ttatcacagg tcctcttttt tttctcttct 540
ccagtttgga gacattaatt agaattctcta agacttcctt tcctgtctga taatcaagca 600
cacaaactca gcctcgtgcc 620

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<210> 57
<211> 878
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(765)
<223>

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<220>
<221> misc_feature
<222> (862)..(862)
<223> At nucleotide 862, n = unknown

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<400> 57
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Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr
1 5 10 15

aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat 96
Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His
20 25 30

ttt gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat 144
Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His
35 40 45

tca gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga 192
Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly
50 55 60

tgc agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc 240
Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile
65 70 75 80

tgt gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt 288
Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe
85 90 95

att ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt 336
Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu
100 105 110

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agt ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg 384
 Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met
 115 120 125

 cct aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc 432
 Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe
 130 135 140

 aca gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata 480
 Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile
 145 150 155 160

 caa atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta 528
 Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val
 165 170 175

 aga agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag 576
 Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
 180 185 190

 tgg agt gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta 624
 Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu
 195 200 205

 gta ttt ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta 672
 Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val
 210 215 220

 ata act tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc 720
 Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile
 225 230 235 240

 ttt cat aca aaa aaa gaa gtc ttt tct cat caa gac aca ttc tgt 765
 Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
 245 250 255

 tgactcagta actttcagtc ttatggccag atgttaaata tgagtcttat taaactgaag 825

 cttttcctca aatattgaat aaatcttatt ttaaaangaa aaaaaaaaaa aaa 878

<210> 58
 <211> 255
 <212> PRT
 <213> Canis familiaris

<400> 58

Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr
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 Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His
 20 25 30

 Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His

35

40

45

Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly
50 55 60

Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile
65 70 75 80

Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe
85 90 95

Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu
100 105 110

Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met
115 120 125

Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe
130 135 140

Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile
145 150 155 160

Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val
165 170 175

Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu
180 185 190

Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu
195 200 205

Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val
210 215 220

Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile
225 230 235 240

Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr Phe Cys
245 250 255

<210> 59

<211> 878

<212> DNA
<213> Canis familiaris

<220>
<221> misc_feature
<222> (17)..(17)
<223> At nucleotide 17, n = unknown

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 atcaagaaaa atactaaggt ttccttccat atgtcacctt tccagcattg ttcatcactc 300
 cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag 360
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 atgggtcctt taggcatgtt ccatttcagg ttaatttcct ctgaattctt cacagtaaga 540
 ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg 600
 ggtctgatag gctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct 660
 gatgactcca aatagggaaa cctgcatccc atattttttc cattaacctt gatgtaatca 720
 gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggta attggtatca 780
 aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca 840
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<212> DNA
<213> Canis familiaris

<220>
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<222> (184)..(1341)
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<220>
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<222> (1438)..(1438)
<223> At nucleotide 1438, n = unknown

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taattcattt cttgagaaac catattattg agtggaact tcaaagtatt gaatcttgga 180
gga atg gct ttc att cat ttg gat gtc gga ttc ctc tat acc ctg ctt 228
Met Ala Phe Ile His Leu Asp Val Gly Phe Leu Tyr Thr Leu Leu
1 5 10 15
gtt tgc aca gca ttt ggc tct atg ctt tca aat gct gag ata aaa gtt 276
Val Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val
20 25 30
aat cct cct cag gat ttt gag ata gtg gac cct gga tat tta ggt tat 324
Asn Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr
35 40 45
ctc tct ttg caa tgg caa cct cca tta ttt ccg gat aat ttt aag gaa 372
Leu Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu
50 55 60
tgc aca ata gaa tat gaa tta aaa tac cga aac att gat agt gaa aac 420
Cys Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn
65 70 75
tgg aag acc atc att acc aag aat cta cat tac aaa gat ggg ttt gat 468
Trp Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp
80 85 90 95
ctt aac aaa ggt att gaa gca aag ata aac aca ctt ctg cca gca caa 516
Leu Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln
100 105 110
tgc aca aat gga tca gaa gtt aga agt tca tgg gca gaa act act tat 564
Cys Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr
115 120 125
tgg aca tca cca caa gga aat cgg gaa act aaa att caa gat atg gac 612
Trp Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp
130 135 140
tgt gta tat tac aac tgg caa tat tta gtc tgc tct tgg aaa cct ggc 660
Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly
145 150 155
atg ggt gtc cat ttt gat acc aat tac cag ttg ttt tac tgg tat gag 708
Met Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu
160 165 170 175
ggc ttg gac cat tca gca gag tgt act gat tac atc aag gtt aat gga 756
Gly Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly
180 185 190
aaa aat atg gga tgc agg ttt ccc tat ttg gag tca tca gac tat aaa 804

Lys	Asn	Met	Gly	Cys	Arg	Phe	Pro	Tyr	Leu	Glu	Ser	Ser	Asp	Tyr	Lys	
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gat	ttc	tac	atc	tgt	gtt	aat	ggg	tca	tca	gaa	tcc	cag	cct	atc	aga	852
Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	
		210					215					220				
ccc	agc	tat	ttt	att	ttt	cag	ctt	caa	aat	ata	gtt	aaa	cct	atg	cca	900
Pro	Ser	Tyr	Phe	Ile	Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	
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cca	gac	tac	ctt	agt	ctt	act	gtg	aag	aat	tca	gag	gaa	att	aac	ctg	948
Pro	Asp	Tyr	Leu	Ser	Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	
240					245					250					255	
aaa	tgg	aac	atg	cct	aaa	gga	ccc	att	cca	gcc	aaa	tgt	ttc	att	tat	996
Lys	Trp	Asn	Met	Pro	Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	
			260					265						270		
gaa	att	gaa	ttc	aca	gag	gat	ggg	act	act	tgg	gtg	act	acc	aca	gtt	1044
Glu	Ile	Glu	Phe	Thr	Glu	Asp	Gly	Thr	Thr	Trp	Val	Thr	Thr	Thr	Val	
			275				280					285				
gag	aat	gag	ata	caa	atc	aca	aga	aca	tca	aat	gaa	agc	caa	aaa	tta	1092
Glu	Asn	Glu	Ile	Gln	Ile	Thr	Arg	Thr	Ser	Asn	Glu	Ser	Gln	Lys	Leu	
		290					295				300					
tgc	ttt	ttg	gta	aga	agt	aaa	gtg	aat	att	tat	tgc	tca	gat	gat	gga	1140
Cys	Phe	Leu	Val	Arg	Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	
	305					310					315					
atc	tgg	agt	gag	tgg	agt	gat	gaa	caa	tgc	tgg	aaa	ggg	gac	ata	tgg	1188
Ile	Trp	Ser	Glu	Trp	Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	
320					325					330					335	
aag	gaa	acc	tta	gta	ttt	ttc	ttg	ata	cca	ttt	gct	ttt	gtc	tca	ata	1236
Lys	Glu	Thr	Leu	Val	Phe	Phe	Leu	Ile	Pro	Phe	Ala	Phe	Val	Ser	Ile	
				340					345					350		
ttt	gtt	ttg	gta	ata	act	tgc	ctg	ctt	ttg	tat	aag	caa	agg	gct	tta	1284
Phe	Val	Leu	Val	Ile	Thr	Cys	Leu	Leu	Leu	Tyr	Lys	Gln	Arg	Ala	Leu	
			355				360						365			
ctg	aaa	acg	atc	ttt	cat	aca	aaa	aaa	gaa	gtc	ttt	tct	cat	caa	gac	1332
Leu	Lys	Thr	Ile	Phe	His	Thr	Lys	Lys	Glu	Val	Phe	Ser	His	Gln	Asp	
		370					375					380				
aca	ttc	tgt	tgactcagta	acttttcagtc	ttatggccag	atgttaaata										1381
Thr	Phe	Cys														
		385														
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aaaaaaaaa	aaa															1454

<211> 386
 <212> PRT
 <213> Canis familiaris

<400> 61

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Cys Thr Ala Phe Gly Ser Met Leu Ser Asn Ala Glu Ile Lys Val Asn
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Pro Pro Gln Asp Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu
 35 40 45

Ser Leu Gln Trp Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys
 50 55 60

Thr Ile Glu Tyr Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp
 65 70 75 80

Lys Thr Ile Ile Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu
 85 90 95

Asn Lys Gly Ile Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys
 100 105 110

Thr Asn Gly Ser Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp
 115 120 125

Thr Ser Pro Gln Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys
 130 135 140

Val Tyr Tyr Asn Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met
 145 150 155 160

Gly Val His Phe Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly
 165 170 175

Leu Asp His Ser Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys
 180 185 190

Asn Met Gly Cys Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp
 195 200 205

Phe Tyr Ile Cys Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro
 210 215 220

Ser Tyr Phe Ile Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro
 225 230 235 240

Asp Tyr Leu Ser Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys
 245 250 255

Trp Asn Met Pro Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu
 260 265 270

Ile Glu Phe Thr Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu
 275 280 285

Asn Glu Ile Gln Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys
 290 295 300

Phe Leu Val Arg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile
 305 310 315 320

Trp Ser Glu Trp Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys
 325 330 335

Glu Thr Leu Val Phe Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe
 340 345 350

Val Leu Val Ile Thr Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu
 355 360 365

Lys Thr Ile Phe His Thr Lys Lys Glu Val Phe Ser His Gln Asp Thr
 370 375 380

Phe Cys
 385

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 <212> DNA
 <213> Canis familiaris

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<223> At nucleotide 17, n = unknown

<400> 62

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gtgtcttgat gagaaaagac ttcttttttt gtatgaaaga tcgttttcag taaagccctt      180
tgcttataca aaagcaggca agttattacc aaaacaaata ttgagacaaa agcaaatggt      240
atcaagaaaa atactaagggt ttccttccat atgtcacctt tccagcattg ttcatcactc      300
cactcactcc agattccatc atctgagcaa taaatattca ctttacttct taccaaaaag      360
cataattttt ggcttttcatt tgatgttctt gtgatttgta tctcattctc aactgtggta      420
gtcacccaag tagtaccatc ctctgtgaat tcaatttcat aaatgaaaca tttggctgga      480
atgggtcctt taggcatggt ccatttcagg ttaatttcct ctgaattctt cacagtaaga      540
ctaaggtagt ctggtggcat aggtttaact atattttgaa gctgaaaaat aaaatagctg      600
ggtctgatag gctgggattc tgatgaccca ttaacacaga tgtagaaatc tttatagtct      660
gatgactcca aatagggaaa cctgcatccc atattttttc cattaacctt gatgtaatca      720
gtacactctg ctgaatggtc caagccctca taccagtaaa acaactggta attggtatca      780
aaatggacac ccatgccagg tttccaagag cagactaaat attgccagtt gtaatataca      840
cagtccatat cttgaatttt agtttccga tttccttggt gtgatgtcca ataagtagtt      900
tctgcccattg aacttctaac ttctgatcca tttgtgcatt gtgctggcag aagtgtgttt      960
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atgatggtct tccagttttc actatcaatg tttcgggtatt ttaattcata ttctattgtg     1080
cattccttaa aattatccgg aaataatgga ggttgccatt gcaaagagag ataacctaaa     1140
tatccagggt ccactatctc aaaatcctga ggaggattaa cttttatctc agcatttgaa     1200
agcatagagc caaatgctgt gcaaacaagc agggatataga ggaatccgac atccaaatga     1260
atgaaagcca ttctccaag attcaatact ttgaagtttc cactcaataa tatggtttct     1320
caagaaatga attatcatag gcaattatca caggctcctc tttttttctc ttctccagtt     1380
tgagacatt aattagaatc tctaagactt cccttctgt ctgataatca agcacacaaa     1440
ctcagcctcg tgcc                                     1454
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<210> 63

<211> 1158

<212> DNA

<213> Canis familiaris

<400> 63

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gaccctggat	atttaggtta	tctctctttg	caatggcaac	ctccattatt	tccggataat	180
tttaaggaat	gcacaataga	atatgaatta	aaataccgaa	acattgatag	tgaaaactgg	240
aagaccatca	ttaccaagaa	tctacattac	aaagatgggt	ttgatcttaa	caaaggtatt	300
gaagcaaaga	ttaacacact	tctgccagca	caatgcacaa	atggatcaga	agttagaagt	360
tcatgggcag	aaactactta	ttggacatca	ccacaaggaa	atcgggaaac	taaaattcaa	420
gatatggact	gtgtatatta	caactggcaa	tatttagtct	gctcttgga	acctggcatg	480
gggtgtccatt	ttgataccaa	ttaccagttg	ttttactggg	atgagggtct	ggaccattca	540
gcagagtgtg	ctgattacat	caaggttaat	ggaaaaata	tgggatgcag	gtttccctat	600
ttggagtcac	cagactataa	agatttctac	atctgtgtta	atgggtcatc	agaatcccag	660
cctatcagac	ccagctattt	tatttttcag	cttcaaaata	tagttaaac	tatgccacca	720
gactacctta	gtcttactgt	gaagaattca	gaggaaatta	acctgaaatg	gaacatgcct	780
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acttgggtga	ctaccacagt	tgagaatgag	atacaaatca	caagaacatc	aatgaaagc	900
caaaaattat	gcttttttgg	aagaagtaaa	gtgaatattt	attgctcaga	tgatggaatc	960
tggagtgagt	ggagtgatga	acaatgctgg	aaagggtgaca	tatggaagga	aaccttagta	1020
tttttcttga	taccatttgc	ttttgtctca	atatttgttt	tggttaatac	ttgcctgctt	1080
ttgtataagc	aaagggtctt	actgaaaacg	atctttcata	caaaaaaaga	agtcttttct	1140
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<210> 64

<211> 1158

<212> DNA

<213> Canis familiaris

<400> 64

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aaatgggtatc	aagaaaaata	ctaagggttc	cttccatatg	tcacctttcc	agcattgttc	180

atcactccac tcactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240
caaaaagcat aatTTTTTggc tttcatttga tgttcttgtg atttgtatct cattctcaac 300
tgtggtagtc acccaagtag taccatcctc tgtgaattca atttcataaa tgaaacattt 360
ggctggaatg ggtccttttag gcatgttcca tttcagggtta atttcctctg aattcttcac 420
agtaagacta aggtagtctg gtggcatagg tttaactata ttttgaagct gaaaaataaa 480
atagctgggt ctgataggct gggattctga tgaccatta acacagatgt agaaatcttt 540
atagtctgat gactccaaat agggaaacct gcatcccata ttttttccat taaccttgat 600
gtaatcagta cactctgctg aatgggtccaa gccctcatac cagtaaaaca actggtaatt 660
ggatatcaaaa tggacacca tgccagggtt ccaagagcag actaaatatt gccagttgta 720
atatacacag tccatatctt gaatttttagt ttcccgattt ccttgtgggtg atgtccaata 780
agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840
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cttggtaatg atggtcttcc agttttcact atcaatgttt cggatatttta attcatattc 960
tattgtgcat tccttaaaat tatccgaaa taatggaggt tgccattgca aagagagata 1020
acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080
atttgaaagc atagagccaa atgctgtgca aacaagcagg gtatagagga atccgacatc 1140
caaatgaatg aaagccat 1158

<210> 65
<211> 1095
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (1)..(1095)
<223>

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gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg caa 96
Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp Gln
20 25 30
cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat gaa 144
Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu

35	40	45	
tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att acc Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile Thr 50 55 60			192
aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att gaa Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu 65 70 75 80			240
gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca gaa Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu 85 90 95			288
gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa gga Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln Gly 100 105 110			336
aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac tgg Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp 115 120 125			384
caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt gat Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp 130 135 140			432
acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca gca Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala 145 150 155 160			480
gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc agg Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg 165 170 175			528
ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt gtt Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val 180 185 190			576
aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att ttt Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe 195 200 205			624
cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt ctt Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu 210 215 220			672
act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct aaa Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys 225 230 235 240			720
gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca gag Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu 245 250 255			768
gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa atc Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile 260 265 270			816

aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga agt 864
 Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser
 275 280 285

aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg agt 912
 Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser
 290 295 300

gat gaa caa tgc tgg aaa ggt gac ata tgg aag gaa acc tta gta ttt 960
 Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe
 305 310 315 320

ttc ttg ata cca ttt gct ttt gtc tca ata ttt gtt ttg gta ata act 1008
 Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr
 325 330 335

tgc ctg ctt ttg tat aag caa agg gct tta ctg aaa acg atc ttt cat 1056
 Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His
 340 345 350

aca aaa aaa gaa gtc ttt tct cat caa gac aca ttc tgt 1095
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 355 360 365

<210> 66

<211> 365

<212> PRT

<213> Canis familiaris

<400> 66

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 20 25 30

Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr Glu
 35 40 45

Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile Thr
 50 55 60

Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu
 65 70 75 80

Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser Glu
 85 90 95

Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln Gly
100 105 110

Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp
115 120 125

Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe Asp
130 135 140

Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser Ala
145 150 155 160

Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys Arg
165 170 175

Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val
180 185 190

Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile Phe
195 200 205

Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser Leu
210 215 220

Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro Lys
225 230 235 240

Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr Glu
245 250 255

Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln Ile
260 265 270

Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg Ser
275 280 285

Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser
290 295 300

Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Leu Val Phe
305 310 315 320

Phe Leu Ile Pro Phe Ala Phe Val Ser Ile Phe Val Leu Val Ile Thr

325

330

335

Cys Leu Leu Leu Tyr Lys Gln Arg Ala Leu Leu Lys Thr Ile Phe His
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355 360 365

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<211> 1095
<212> DNA
<213> Canis familiaris

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aaatgggtatc aagaaaaata ctaagggttc cttccatatg tcacctttcc agcattgttc 180
atcactccac tcactccaga ttccatcatc tgagcaataa atattcactt tacttcttac 240
caaaaagcat aattttttggc tttcatttga tgttcttgtg atttgtatct cattctcaac 300
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ggctggaatg ggtccttttag gcatgttcca tttcagggtta atttcctctg aattccttcac 420
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atagtctgat gactccaaat agggaaacct gcatccata ttttttccat taaccttgat 600
gtaatcagta cactctgctg aatgggtcaa gccctcatac cagtaaaaaca actggtaatt 660
ggatatcaaaa tggacacca tgccagggtt ccaagagcag actaaatatt gccagttgta 720
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agtagtttct gcccatgaac ttctaacttc tgatccattt gtgcattgtg ctggcagaag 840
tgtgtttatc tttgcttcaa tacctttggt aagatcaaac ccatctttgt aatgtagatt 900
cttggtaatg atggtcttcc agttttcact atcaatgttt cggatatttta attcatattc 960
tattgtgcat tccttaaaat tatccgaaa taatggaggt tgccattgca aagagagata 1020
acctaaatat ccagggtcca ctatctcaaa atcctgagga ggattaactt ttatctcagc 1080
atttgaaagc ataga 1095

<210> 68

<211> 954
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 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(954)
 <223>

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 ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96
 Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
 20 25 30
 caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144
 Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
 35 40 45
 gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192
 Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
 50 55 60
 acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240
 Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
 65 70 75 80
 gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288
 Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
 85 90 95
 gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa 336
 Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
 100 105 110
 gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac 384
 Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
 115 120 125
 tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt 432
 Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
 130 135 140
 gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca 480
 Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
 145 150 155 160
 gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc 528
 Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
 165 170 175
 agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt 576
 Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys

180										185					190					
gtt	aat	ggg	tca	tca	gaa	tcc	cag	cct	atc	aga	ccc	agc	tat	ttt	att	624				
Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile					
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ttt	cag	ctt	caa	aat	ata	gtt	aaa	cct	atg	cca	cca	gac	tac	ctt	agt	672				
Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser					
210			215					220												
ctt	act	gtg	aag	aat	tca	gag	gaa	att	aac	ctg	aaa	tgg	aac	atg	cct	720				
Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro					
225		230					235								240					
aaa	gga	ccc	att	cca	gcc	aaa	tgt	ttc	att	tat	gaa	att	gaa	ttc	aca	768				
Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	Glu	Ile	Glu	Phe	Thr					
245					250					255										
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Glu	Asp	Gly	Thr	Thr	Trp	Val	Thr	Thr	Thr	Val	Glu	Asn	Glu	Ile	Gln					
260				265					270											
atc	aca	aga	aca	tca	aat	gaa	agc	caa	aaa	tta	tgc	ttt	ttg	gta	aga	864				
Ile	Thr	Arg	Thr	Ser	Asn	Glu	Ser	Gln	Lys	Leu	Cys	Phe	Leu	Val	Arg					
275			280					285												
agt	aaa	gtg	aat	att	tat	tgc	tca	gat	gat	gga	atc	tgg	agt	gag	tgg	912				
Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp					
290		295					300													
agt	gat	gaa	caa	tgc	tgg	aaa	ggg	gat	atc	tgg	aag	gaa	acc			954				
Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr							
305		310					315													

<210> 69
 <211> 318
 <212> PRT
 <213> Canis familiaris

<400> 69

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Phe	Glu	Ile	Val	Asp	Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Ser	Leu	Gln	Trp
			20					25					30		
Gln	Pro	Pro	Leu	Phe	Pro	Asp	Asn	Phe	Lys	Glu	Cys	Thr	Ile	Glu	Tyr
		35					40					45			
Glu	Leu	Lys	Tyr	Arg	Asn	Ile	Asp	Ser	Glu	Asn	Trp	Lys	Thr	Ile	Ile
	50					55					60				

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
180 185 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
195 200 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
245 250 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg
275 280 285

Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
 290 295 300

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr
 305 310 315

<210> 70
 <211> 954
 <212> DNA
 <213> Canis familiaris

<400> 70
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 atttgatgtt cttgtgattt gtatctcatt ctcaactgtg gtagtcaccc aagtagtacc 180
 atcctctgtg aattcaattt cataaatgaa acatttggct ggaatgggtc ctttaggcat 240
 gttccatttc aggttaattt cctctgaatt cttcacagta agactaaggt agtctgggtg 300
 cataggttta actatatattt gaagctgaaa aataaaatag ctgggtctga taggctggga 360
 ttctgatgac ccattaacac agatgtagaa atctttatag tctgatgact ccaaataagg 420
 aaacctgcat cccatatattt ttccattaac cttgatgtaa tcagtacact ctgctgaatg 480
 gtccaagccc tcataaccagt aaaacaactg gtaattggta tcaaatgga caccatgcc 540
 aggtttccaa gagcagacta aatattgcca gttgtaatat acacagtcca tatcttgaat 600
 tttagtttcc cgatttcctt gtgggtgatgt ccaataagta gtttctgccc atgaacttct 660
 aacttctgat ccatttgtgc attgtgctgg cagaagtgtg tttatctttg cttcaatacc 720
 tttgttaaga tcaaaccat ctttgtaatg tagattcttg gtaatgatgg tcttccagtt 780
 ttcactatca atgtttcggg attttaattc atattctatt gtgcattcct taaaattatc 840
 cggaataaat ggaggttgcc attgcaaaga gagataacct aaatatccag ggtccactat 900
 ctcaaatcc tgaggaggat taacttttat ctcagcattt gaaagcatag acat 954

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 <211> 1686
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
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 <223>

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ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
20 25 30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
35 40 45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
85 90 95

gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa 336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac 384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
115 120 125

tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt 432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
130 135 140

gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca 480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145 150 155 160

gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc 528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
165 170 175

agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt 576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
180 185 190

gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att 624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
195 200 205

ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt 672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
210 215 220

ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro 225 230 235 240	720
aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr 245 250 255	768
gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln 260 265 270	816
atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg 275 280 285	864
agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp 290 295 300	912
agt gat gaa caa tgc tgg aaa ggt gat atc tgg aag gaa acc gga tcc Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser 305 310 315 320	960
aac act aaa gta gac aag cca gtg ttc aat gaa tgc aga tgc act gat Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp 325 330 335	1008
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atc ttt ccc ccg aaa ccc aag gac atc ctc agg att acc cga aca ccc Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro 355 360 365	1104
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cag atc agc tgg ttc gtg gat ggt aag gag gtg cac aca gcc aag acc Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr 385 390 395 400	1200
cag tct cgt gag cag cag ttc aac ggc acc tac cgt gtg gtc agc gtc Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val 405 410 415	1248
ctc ccc att gag cac cag gac tgg ctc aca ggg aag gag ttc aag tgc Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys 420 425 430	1296
aga gtc aac cac ata gac ctc ccg tct ccc atc gag agg acc atc tct Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser 435 440 445	1344

aag gcc aga ggg agg gcc cat aag ccc agt gtg tat gtc ctg ccg cca	1392
Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro	
450 455 460	
tcc cca aag gag ttg tca tcc agt gac aca gtc agc atc acc tgc ctg	1440
Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu	
465 470 475 480	
ata aaa gac ttc tac cca cct gac att gat gtg gag tgg cag agc aat	1488
Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn	
485 490 495	
gga cag cag gag ccc gag agg aag cac cgc atg acc ccg ccc cag ctg	1536
Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu	
500 505 510	
gac gag gac ggg tcc tac ttc ctg tac agc aag ctc tct gtg gac aag	1584
Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys	
515 520 525	
agc cgc tgg cag cag gga gac ccc ttc aca tgt gcg gtg atg cat gaa	1632
Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu	
530 535 540	
act cta cag aac cac tac aca gat cta tcc ctc tcc cat tct ccg ggt	1680
Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly	
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aaa tga	1686
Lys	

<210> 72
 <211> 561
 <212> PRT
 <213> Canis familiaris

<400> 72

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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
20 25 30

Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
35 40 45

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile

65				70				75				80			
Glu	Ala	Lys	Ile	Asn 85	Thr	Leu	Leu	Pro	Ala 90	Gln	Cys	Thr	Asn	Gly 95	Ser
Glu	Val	Arg	Ser 100	Ser	Trp	Ala	Glu	Thr 105	Thr	Tyr	Trp	Thr	Ser 110	Pro	Gln
Gly	Asn	Arg 115	Glu	Thr	Lys	Ile	Gln 120	Asp	Met	Asp	Cys	Val 125	Tyr	Tyr	Asn
Trp	Gln 130	Tyr	Leu	Val	Cys	Ser 135	Trp	Lys	Pro	Gly	Met 140	Gly	Val	His	Phe
Asp 145	Thr	Asn	Tyr	Gln	Leu 150	Phe	Tyr	Trp	Tyr	Glu 155	Gly	Leu	Asp	His	Ser 160
Ala	Glu	Cys	Thr	Asp 165	Tyr	Ile	Lys	Val	Asn 170	Gly	Lys	Asn	Met	Gly 175	Cys
Arg	Phe	Pro	Tyr 180	Leu	Glu	Ser	Ser	Asp 185	Tyr	Lys	Asp	Phe	Tyr 190	Ile	Cys
Val	Asn	Gly 195	Ser	Ser	Glu	Ser	Gln 200	Pro	Ile	Arg	Pro	Ser 205	Tyr	Phe	Ile
Phe 210	Gln	Leu	Gln	Asn	Ile	Val 215	Lys	Pro	Met	Pro	Pro 220	Asp	Tyr	Leu	Ser
Leu 225	Thr	Val	Lys	Asn 230	Ser	Glu	Glu	Ile	Asn 235	Leu	Lys	Trp	Asn	Met	Pro 240
Lys	Gly	Pro	Ile	Pro 245	Ala	Lys	Cys	Phe	Ile 250	Tyr	Glu	Ile	Glu	Phe	Thr
Glu	Asp	Gly	Thr 260	Thr	Trp	Val	Thr	Thr 265	Thr	Val	Glu	Asn	Glu 270	Ile	Gln
Ile	Thr	Arg 275	Thr	Ser	Asn	Glu	Ser 280	Gln	Lys	Leu	Cys	Phe 285	Leu	Val	Arg
Ser	Lys 290	Val	Asn	Ile	Tyr	Cys 295	Ser	Asp	Asp	Gly	Ile 300	Trp	Ser	Glu	Trp

Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
305 310 315 320

Asn Thr Lys Val Asp Lys Pro Val Phe Asn Glu Cys Arg Cys Thr Asp
325 330 335

Thr Pro Pro Cys Pro Val Pro Glu Pro Leu Gly Gly Pro Ser Val Leu
340 345 350

Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Arg Ile Thr Arg Thr Pro
355 360 365

Glu Val Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
370 375 380

Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
385 390 395 400

Gln Ser Arg Glu Gln Gln Phe Asn Gly Thr Tyr Arg Val Val Ser Val
405 410 415

Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
420 425 430

Arg Val Asn His Ile Asp Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
435 440 445

Lys Ala Arg Gly Arg Ala His Lys Pro Ser Val Tyr Val Leu Pro Pro
450 455 460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Ser Ile Thr Cys Leu
465 470 475 480

Ile Lys Asp Phe Tyr Pro Pro Asp Ile Asp Val Glu Trp Gln Ser Asn
485 490 495

Gly Gln Gln Glu Pro Glu Arg Lys His Arg Met Thr Pro Pro Gln Leu
500 505 510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
515 520 525

Ser Arg Trp Gln Gln Gly Asp Pro Phe Thr Cys Ala Val Met His Glu
530 535 540

Thr Leu Gln Asn His Tyr Thr Asp Leu Ser Leu Ser His Ser Pro Gly
545 550 555 560

Lys

<210> 73
<211> 1686
<212> DNA
<213> Canis familiaris

<400> 73
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gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcatgc ggtgcttcct 180
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ctgggtgctca atggggagga cgctgaccac acggtagggtg ccgttgaact gctgctcacg 480
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gtagtctggt ggcatagggt taactatatt ttgaagctga aaaataaaat agctgggtct 1080
gataggctgg gattctgatg acccattnaac acagatgtag aaatctttat agtctgatga 1140

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ctccaaatag ggaaacctgc atcccatatt ttttccatta accttgatgt aatcagtaca 1200
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gacacccatg ccaggtttcc aagagcagac taaatattgc cagttgtaat atacacagtc 1320
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ccatgaactt ctaacttctg atccatttgt gcattgtgct ggcagaagtg tgtttatctt 1440
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cttaaaatta tccggaaata atggagggtg ccattgcaaa gagagataac ctaaatatcc 1620
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agacat 1686

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<210> 74
<211> 1698
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(1695)
<223>

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ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg 96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
20 25 30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
35 40 45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca 288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
85 90 95

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Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
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gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
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tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
130 135 140	
gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
145 150 155 160	
gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	
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agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt	576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys	
180 185 190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att	624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile	
195 200 205	
ttt cag ctt caa aat ata gtt aaa cct atg cca cca gac tac ctt agt	672
Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser	
210 215 220	
ctt act gtg aag aat tca gag gaa att aac ctg aaa tgg aac atg cct	720
Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro	
225 230 235 240	
aaa gga ccc att cca gcc aaa tgt ttc att tat gaa att gaa ttc aca	768
Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr	
245 250 255	
gag gat ggt act act tgg gtg act acc aca gtt gag aat gag ata caa	816
Glu Asp Gly Thr Thr Trp Val Thr Thr Val Glu Asn Glu Ile Gln	
260 265 270	
atc aca aga aca tca aat gaa agc caa aaa tta tgc ttt ttg gta aga	864
Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg	
275 280 285	
agt aaa gtg aat att tat tgc tca gat gat gga atc tgg agt gag tgg	912
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp	
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Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser	
305 310 315 320	
aac act aaa gta gac aag cca gtg ccc aaa aga gaa aat gga aga gtt	1008

Asn Thr Lys Val Asp Lys Pro Val Pro Lys Arg Glu Asn Gly Arg Val	
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cct cgc cca cct gat tgt ccc aaa tgc cca gcc cct gaa atg ctg gga	1056
Pro Arg Pro Pro Asp Cys Pro Lys Cys Pro Ala Pro Glu Met Leu Gly	
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Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu Leu	
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Ile Ala Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Leu Asp Pro	
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Glu Asp Pro Glu Val Gln Ile Ser Trp Phe Val Asp Gly Lys Gln Met	
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caa aca gcc aag act cag cct cgt gag gag cag ttc aat ggc acc tac	1248
Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr	
405 410 415	
cgt gtg gtc agt gtc ctc ccc att ggg cac cag gac tgg ctc aag ggg	1296
Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly	
420 425 430	
aag cag ttc acg tgc aaa gtc aac aac aaa gcc ctc cca tcc ccg atc	1344
Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile	
435 440 445	
gag agg acc atc tcc aag gcc aga ggg caa gcc cat cag ccc agt gtg	1392
Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val	
450 455 460	
tat gtc ctg ccg cca tcc cgg gag gag ttg agc aag aac aca gtc agc	1440
Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser	
465 470 475 480	
ttg aca tgc ctg atc aaa gac ttc ttc cca cct gac att gat gtg gag	1488
Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu	
485 490 495	
tgg cag agc aat gga cag cag gag cct gag agc aag tac cgc acg acc	1536
Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr	
500 505 510	
ccg ccc cag ctg gac gag gac ggg tcc tac ttc ctg tac agc aag ctc	1584
Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu	
515 520 525	
tct gtg gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg	1632
Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala	
530 535 540	
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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
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50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
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Val	Asn	Gly	Ser	Ser	Glu	Ser	Gln	Pro	Ile	Arg	Pro	Ser	Tyr	Phe	Ile	
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Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser	
	210					215					220					
Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro	
225					230					235					240	
Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	Glu	Ile	Glu	Phe	Thr	
				245					250					255		
Glu	Asp	Gly	Thr	Thr	Trp	Val	Thr	Thr	Thr	Val	Glu	Asn	Glu	Ile	Gln	
			260					265					270			
Ile	Thr	Arg	Thr	Ser	Asn	Glu	Ser	Gln	Lys	Leu	Cys	Phe	Leu	Val	Arg	
		275					280					285				
Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	
	290					295					300					
Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr	Gly	Ser	
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Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Pro	Lys	Arg	Glu	Asn	Gly	Arg	Val	
				325					330					335		
Pro	Arg	Pro	Pro	Asp	Cys	Pro	Lys	Cys	Pro	Ala	Pro	Glu	Met	Leu	Gly	
			340					345					350			
Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Leu	
		355					360					365				
Ile	Ala	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Leu	Asp	Pro	
	370					375					380					
Glu	Asp	Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Gly	Lys	Gln	Met	
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Gln Thr Ala Lys Thr Gln Pro Arg Glu Glu Gln Phe Asn Gly Thr Tyr
405 410 415

Arg Val Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Lys Gly
420 425 430

Lys Gln Phe Thr Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile
435 440 445

Glu Arg Thr Ile Ser Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val
450 455 460

Tyr Val Leu Pro Pro Ser Arg Glu Glu Leu Ser Lys Asn Thr Val Ser
465 470 475 480

Leu Thr Cys Leu Ile Lys Asp Phe Phe Pro Pro Asp Ile Asp Val Glu
485 490 495

Trp Gln Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Thr Thr
500 505 510

Pro Pro Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu
515 520 525

Ser Val Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala
530 535 540

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Glu Ser Leu Ser
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His Ser Pro Gly Lys
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<210> 76

<211> 1698

<212> DNA

<213> Canis familiaris

<400> 76

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gctgtacagg aagtaggacc cgtcctcgtc cagctggggc ggggtcgtgc ggtacttgct 180

ctcaggctcc tgctgtccat tgctctgcca ctccacatca atgtcagggtg ggaagaagtc 240

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tgtggtagtc acccaagtag taccatcttc tgtgaattca atttcataaa tgaaacattt	960
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gtaatcagta cactctgctg aatgggtcaa gccctcatal cagtaaaaca actggtaatt	1260
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tattgtgcat tccttaaaat tatccgaaa taatggagggt tgccattgca aagagagata	1620
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<210> 77
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<400> 77

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ttt gag ata gtg gac cct gga tat tta ggt tat ctc tct ttg caa tgg	96
Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp	
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caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat	144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr	
35 40 45	
gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att	192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile	
50 55 60	
acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att	240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile	
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gaa gca aag ata aac aca ctt ctg cca gca caa tgc aca aat gga tca	288
Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser	
85 90 95	
gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa	336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
100 105 110	
gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
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tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
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Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
145 150 155 160	
gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	
165 170 175	
agg ttt ccc tat ttg gag tca tca gac tat aaa gat ttc tac atc tgt	576
Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys	
180 185 190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att	624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile	

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Phe	Gln	Leu	Gln	Asn	Ile	Val	Lys	Pro	Met	Pro	Pro	Asp	Tyr	Leu	Ser	
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Leu	Thr	Val	Lys	Asn	Ser	Glu	Glu	Ile	Asn	Leu	Lys	Trp	Asn	Met	Pro	
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aaa	gga	ccc	att	cca	gcc	aaa	tgt	ttc	att	tat	gaa	att	gaa	ttc	aca	768
Lys	Gly	Pro	Ile	Pro	Ala	Lys	Cys	Phe	Ile	Tyr	Glu	Ile	Glu	Phe	Thr	
245					250					255						
gag	gat	ggt	act	act	tgg	gtg	act	acc	aca	gtt	gag	aat	gag	ata	caa	816
Glu	Asp	Gly	Thr	Thr	Trp	Val	Thr	Thr	Thr	Val	Glu	Asn	Glu	Ile	Gln	
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Ile	Thr	Arg	Thr	Ser	Asn	Glu	Ser	Gln	Lys	Leu	Cys	Phe	Leu	Val	Arg	
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Ser	Lys	Val	Asn	Ile	Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	
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Ser	Asp	Glu	Gln	Cys	Trp	Lys	Gly	Asp	Ile	Trp	Lys	Glu	Thr	Gly	Ser	
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Asn	Thr	Lys	Val	Asp	Lys	Pro	Val	Ala	Lys	Glu	Cys	Glu	Cys	Lys	Cys	
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Asn	Cys	Asn	Asn	Cys	Pro	Cys	Pro	Gly	Cys	Gly	Leu	Leu	Gly	Gly	Pro	
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Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Ile	Leu	Val	Thr	Ala	
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Arg	Thr	Pro	Thr	Val	Thr	Cys	Val	Val	Val	Asp	Leu	Asp	Pro	Glu	Asn	
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Pro	Glu	Val	Gln	Ile	Ser	Trp	Phe	Val	Asp	Ser	Lys	Gln	Val	Gln	Thr	
385					390					395					400	
gcc	aac	acg	cag	cct	cgt	gag	gag	cag	tcc	aat	ggc	acc	tac	cgt	gtg	1248
Ala	Asn	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Ser	Asn	Gly	Thr	Tyr	Arg	Val	
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gtc	agt	gtc	ctc	ccc	att	ggg	cac	cag	gac	tgg	ctt	tca	ggg	aag	cag	1296
Val	Ser	Val	Leu	Pro	Ile	Gly	His	Gln	Asp	Trp	Leu	Ser	Gly	Lys	Gln	
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Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu	
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Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val	
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ctg ccg cca tcg cgg gat gag atg agc aag aat acg gtc acc ctg acc	1440
Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr	
465 470 475 480	
tgt ctg gtc aaa gac ttc ttc cca cct gag att gat gtg gag tgg cag	1488
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln	
485 490 495	
agc aat gga cag cag gag cct gag agc aag tac cgc atg acc ccg ccc	1536
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro	
500 505 510	
cag ctg gat gaa gat ggg tcc tac ttc cta tac agc aag ctc tcc gtg	1584
Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val	
515 520 525	
gac aag agc cgc tgg cag cgg gga gac acc ttc ata tgt gcg gtg atg	1632
Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met	
530 535 540	
cat gaa gct cta cac aac cac tac aca cag ata tcc ctc tcc cat tct	1680
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545 550 555 560	
ccg ggt aaa tga	1692
Pro Gly Lys	

<210> 78
 <211> 563
 <212> PRT
 <213> Canis familiaris

<400> 78

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Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr	
35 40 45	

Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

Glu Ala Lys Ile Asn Thr Leu Leu Pro Ala Gln Cys Thr Asn Gly Ser
85 90 95

Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln
100 105 110

Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn
115 120 125

Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe
130 135 140

Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser
145 150 155 160

Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys
165 170 175

Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys
180 185 190

Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile
195 200 205

Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser
210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
225 230 235 240

Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr
245 250 255

Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln
260 265 270

Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg

275		280		285
Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp				
290		295		300
Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser				
305		310		315 320
Asn Thr Lys Val Asp Lys Pro Val Ala Lys Glu Cys Glu Cys Lys Cys				
	325		330	335
Asn Cys Asn Asn Cys Pro Cys Pro Gly Cys Gly Leu Leu Gly Gly Pro				
	340		345	350
Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Ile Leu Val Thr Ala				
	355		360	365
Arg Thr Pro Thr Val Thr Cys Val Val Val Asp Leu Asp Pro Glu Asn				
	370		375	380
Pro Glu Val Gln Ile Ser Trp Phe Val Asp Ser Lys Gln Val Gln Thr				
385		390		395 400
Ala Asn Thr Gln Pro Arg Glu Glu Gln Ser Asn Gly Thr Tyr Arg Val				
	405		410	415
Val Ser Val Leu Pro Ile Gly His Gln Asp Trp Leu Ser Gly Lys Gln				
	420		425	430
Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro Ser Pro Ile Glu Glu				
	435		440	445
Ile Ile Ser Lys Thr Pro Gly Gln Ala His Gln Pro Asn Val Tyr Val				
	450		455	460
Leu Pro Pro Ser Arg Asp Glu Met Ser Lys Asn Thr Val Thr Leu Thr				
465		470		475 480
Cys Leu Val Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln				
	485		490	495
Ser Asn Gly Gln Gln Glu Pro Glu Ser Lys Tyr Arg Met Thr Pro Pro				
	500		505	510

Gln Leu Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val
515 520 525

Asp Lys Ser Arg Trp Gln Arg Gly Asp Thr Phe Ile Cys Ala Val Met
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545 550 555 560

Pro Gly Lys

<210> 79
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Phe Glu Ile Val Asp Pro Gly Tyr Leu Gly Tyr Leu Ser Leu Gln Trp
20 25 30

caa cct cca tta ttt ccg gat aat ttt aag gaa tgc aca ata gaa tat 144
Gln Pro Pro Leu Phe Pro Asp Asn Phe Lys Glu Cys Thr Ile Glu Tyr
35 40 45

gaa tta aaa tac cga aac att gat agt gaa aac tgg aag acc atc att 192
Glu Leu Lys Tyr Arg Asn Ile Asp Ser Glu Asn Trp Lys Thr Ile Ile
50 55 60

acc aag aat cta cat tac aaa gat ggg ttt gat ctt aac aaa ggt att 240
Thr Lys Asn Leu His Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile
65 70 75 80

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85 90 95	
gaa gtt aga agt tca tgg gca gaa act act tat tgg aca tca cca caa	336
Glu Val Arg Ser Ser Trp Ala Glu Thr Thr Tyr Trp Thr Ser Pro Gln	
100 105 110	
gga aat cgg gaa act aaa att caa gat atg gac tgt gta tat tac aac	384
Gly Asn Arg Glu Thr Lys Ile Gln Asp Met Asp Cys Val Tyr Tyr Asn	
115 120 125	
tgg caa tat tta gtc tgc tct tgg aaa cct ggc atg ggt gtc cat ttt	432
Trp Gln Tyr Leu Val Cys Ser Trp Lys Pro Gly Met Gly Val His Phe	
130 135 140	
gat acc aat tac cag ttg ttt tac tgg tat gag ggc ttg gac cat tca	480
Asp Thr Asn Tyr Gln Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ser	
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gca gag tgt act gat tac atc aag gtt aat gga aaa aat atg gga tgc	528
Ala Glu Cys Thr Asp Tyr Ile Lys Val Asn Gly Lys Asn Met Gly Cys	
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Arg Phe Pro Tyr Leu Glu Ser Ser Asp Tyr Lys Asp Phe Tyr Ile Cys	
180 185 190	
gtt aat ggg tca tca gaa tcc cag cct atc aga ccc agc tat ttt att	624
Val Asn Gly Ser Ser Glu Ser Gln Pro Ile Arg Pro Ser Tyr Phe Ile	
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Phe Gln Leu Gln Asn Ile Val Lys Pro Met Pro Pro Asp Tyr Leu Ser	
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Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro	
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Lys Gly Pro Ile Pro Ala Lys Cys Phe Ile Tyr Glu Ile Glu Phe Thr	
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Glu Asp Gly Thr Thr Trp Val Thr Thr Thr Val Glu Asn Glu Ile Gln	
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Ile Thr Arg Thr Ser Asn Glu Ser Gln Lys Leu Cys Phe Leu Val Arg	
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Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp	
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Lys																	
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210 215 220

Leu Thr Val Lys Asn Ser Glu Glu Ile Asn Leu Lys Trp Asn Met Pro
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Ser Lys Val Asn Ile Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp
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Ser Asp Glu Gln Cys Trp Lys Gly Asp Ile Trp Lys Glu Thr Gly Ser
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Glu Ile Thr Cys Val Val Leu Asp Leu Gly Arg Glu Asp Pro Glu Val
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Gln Ile Ser Trp Phe Val Asp Gly Lys Glu Val His Thr Ala Lys Thr
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Gln Pro Arg Glu Gln Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
405 410 415

Leu Pro Ile Glu His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys
420 425 430

Arg Val Asn His Ile Gly Leu Pro Ser Pro Ile Glu Arg Thr Ile Ser
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Lys Ala Arg Gly Gln Ala His Gln Pro Ser Val Tyr Val Leu Pro Pro
450 455 460

Ser Pro Lys Glu Leu Ser Ser Ser Asp Thr Val Thr Leu Thr Cys Leu
465 470 475 480

Ile Lys Asp Phe Phe Pro Pro Glu Ile Asp Val Glu Trp Gln Ser Asn
485 490 495

Gly Gln Pro Glu Pro Glu Ser Lys Tyr His Thr Thr Ala Pro Gln Leu
500 505 510

Asp Glu Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Ser Val Asp Lys
515 520 525

Ser Arg Trp Gln Gln Gly Asp Thr Phe Thr Cys Ala Val Met His Glu
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<212> DNA
<213> Canis familiaris

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<212> DNA

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<212> DNA

<213> Artificial sequence

<220>

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<400> 90

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<210> 91

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gctatcggat gcttatatac ctttctgata agcacaacat ttggctgtac ttcattctca	180
gacaccgaga taaaagttaa cctcctcag gatTTTgaga tagtggatcc cggatactta	240
ggttatctct atttgcaatg gcaaccccc ctgtctctgg atcattttaa ggaatgcaca	300
gtggaatatg aactaaaata ccgaaacatt ggtagtgaac catggaagac catcattact	360
aagaatctac attacaaaga tgggtttgat cttacaagg gcattgaagc gaagatacac	420

acgcttttac	catggcaatg	cacaaatgga	tcagaagttc	aaagttcctg	ggcagaaact	480
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accaattaca	acttgtttta	ctggtatgag	ggcttggatc	atgcattaca	gtgtgttgat	660
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<210> 97
 <211> 1525
 <212> DNA
 <213> Canis familiaris

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attcctcttc	actccattcg
atcttataaa	aaagcatagg
ttttgtctgt	ggcagactcc
aacaccttgg	tggaatgggt

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<210> 98
 <211> 1369
 <212> DNA
 <213> Canis familiaris

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gtcgggtttc atttgttgtt ttcaagggtg atgtttcatt ttcaactgta gcagtcacca	420
aggtagtatc atcttctctg atctcaattt cataatcaaa acaccttgct ggaataggtc	480

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<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 99
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<210> 100
<211> 27
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<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 100
agtcagagca aaggaacaac caatgtg 27

<210> 101

<211> 21
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<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 101
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<210> 102
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<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

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<223> Synthetic Primer

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<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 104
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